

SEQUENCE LISTING



(1) GENERAL INFORMATION:

(i) APPLICANT: Jacobs, Kenneth
McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa A.
Evans, Cheryl
Merberg, David
Treacy, Maurice
Spaulding, Vikki

(ii) TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM

(iii) NUMBER OF SEQUENCES: 219

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genetics Institute, Inc.
(B) STREET: 87 CambridgePark Drive
(C) CITY: Cambridge
(D) STATE: MA
(E) COUNTRY: U.S.A.
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Sprunger, Suzanne A.
(B) REGISTRATION NUMBER: 41,323

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1800 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | | | | | |
|-------------|--------------|-------------|-------------|------------|--------------------------|------|
| TTTTTTTTTT | TACAGACTTC | ACAGAGAATG | CAGTTGTCTT | GACTTCAGGT | CTGTCTGTTC | 60 |
| TGTTGGCAAG | TAAATGCAGT | ACTGTTCTGA | TCCCGCTGCT | ATTAGAATGC | ATTGTGAAAC | 120 |
| GA CTGGAGTA | TGATTA AAAAG | TTGTGTTCCC | CAATGCTTGG | AGTAGTGATT | GTTGAAGGAA | 180 |
| AAAATCCAGC | TGAGTGATAA | AGGCTGAGTG | TTGAGGAAAT | TTCTGCAGTT | TTAAGCAGTC | 240 |
| GTATTTGTGA | TTGAAGCTGA | GTACATTTTG | CTGGTGTATT | TTTAGGTAAA | ATGCTTTTTG | 300 |
| TTCATTTCTG | GTGGTGGGAG | GGGACTGAAG | CCTTTAGTCT | TTCCAGATG | CAACCTTAAA | 360 |
| ATCAGTGACA | AGAAACATTC | CAAACAAGCA | ACAGTCTTCA | AGAAATTAAA | CTGGCAAGTG | 420 |
| GAAATGTTTA | AACAGTTCAG | TGATCTTTAG | TGCATTGTTT | ATGTGTGGGT | TTCTCTCTCC | 480 |
| CCTCCCTTGG | TCTTAATTCT | TACATGCAGG | AACACTCAGC | AGACACACGT | ATGCGAAGGG | 540 |
| CCAGAGAAGC | CAGACCCAGT | AAGAAAAAAT | AGCCTATTTA | CTTTAAATAA | ACCAAACATT | 600 |
| CCATTTTAAA | TGTGGGGATT | GGGAACCACT | AGTTCTTTCA | GATGGTATTC | TTCAGACTAT | 660 |
| AGAAGGAGCT | TCCAGTTGAA | TTCAACAGTG | GACAAAATGA | GGAAAACAGG | TGAACAAGCT | 720 |
| TTTTCTGTAT | TTACATACAA | AGTCAGATCA | GTTATGGGAC | AATAGTATTG | AATAGATTTT | 780 |
| AGCTTTATGC | TGGAGTAACT | GGCATGTGAG | CAAAGTGTGT | TGGCGTGGGG | GTGGAGGGGT | 840 |
| GAGGTGGGCG | CTAAGCTTTT | TTTAAGATTT | TTCAAGGTACC | CTTCACTAAA | GGCACCGAAG | 900 |
| GCTTAAAGTA | GGACAACCAT | GGAGCTTCCT | GTGGCAGGAG | AGACAACAAA | GCGCTATTAT | 960 |
| CCTAAGGTCA | AGAGAAGTGT | CAGCCTCACC | TGATTTTTAT | TAGTAATGAG | GA CTTCCTC | 1020 |
| AACTCCCTCT | TTCTGGAGTG | AAGCATCCGA | AGGAATGCTT | GAAGTACCCC | TGGGCTTCTC | 1080 |
| TTAACATTTA | AGCAAGCTGT | TTTTATAGCA | GCTCTTAATA | ATAAAGCCCA | AATCTCAAGC | 1140 |
| GGTGCTTGAA | GGGGAGGGAA | AGGGGGAAAAG | CGGGCAACCA | CTTTTCCCTA | GCTTTTCCAG | 1200 |
| AAGCCTGTTA | AAAGCAAGGT | CTCCCCACAA | GCAACTTCTC | TGCCACATCG | CCACCCCGTG | 1260 |
| CCTTTTGATC | TAGCACAGAC | CCTTCACCCC | TCACCTCGAT | GCAGCCAGTA | GCTTGATCC | 1320 |
| TTGTGGGCAT | GATCCATAAT | CGGTTTCAAG | GTAACGATGG | TGTCGAGKTC | TTTGGTGGGT | 1380 |
| TGA ACTATGT | TAGAAAAGGC | CATTAATTTG | CCTGCAAATT | GTTAACAGAA | GGGTATTAAA | 1440 |
| ACCACAGCTA | AGTAGCTCTA | TTATAATACT | TATCCAGTGA | CTAAAACCAA | CTTAAAC ³ CAG | 1500 |
| TAAGTGGAGA | AATAACATGT | TCAAGAACTG | TAATGCTGGG | TGGGAACATG | TA ACTTG TAG | 1560 |
| ACTGGAGAAG | ATAGGCATTT | GAGTGGCTGA | GAGGGCTTTT | GGGTGGGAAT | GCAAAAATTC | 1620 |

TCTGCTAAGA CTTTTTCAGG TGAACATAAC AGACTTGGCC AAGCTAGCAT CTTAGCGGAA 1680
 GCTGATCTCC AATGCTCTTC AGTAGGGTCA TGAAGGTTTT TCTTTTCCTG AGAAAAACAAC 1740
 ACGTATTGTT TTCTCAGGTT TTGCTTTTTG GCCTTTTTCT AGCTTAAAAA AAAAAAAAAA 1800

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Trp Val Ser Leu Ser Pro Pro Leu Val Leu Ile Leu Thr Cys Arg
 1 5 10 15
 Asn Thr Gln Gln Thr His Val Cys Glu Gly Pro Glu Lys Pro Asp Pro
 20 25 30
 Val Arg Lys Asn Ser Leu Phe Thr Leu Asn Lys Pro Asn Ile Pro Phe
 35 40 45

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1063 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAAGTTCCAT CTCTAGAACT GATTTTTATC CGTTCGTGTTT TTCAGGTCTT ATCTGTGTTA 60
 GTTGTGTGTT ACTATCAGGA GGCCCCCTTT GGACCCAGTG GATACAGATT ACGACTCTTC 120
 TTTTATGGTG TATGCAATGT CATTTCTATC ACTTGTGCTT ATACATCATT TTCAATAGTT 180
 CCTCCCAGCA ATGGGACCAC TATGTGGAGA GCCACAATA CAGTCTTCAG TGCCATTTTG 240
 GCTTTTTTAC TCGTAGATGA GAAAATGGCT TATGTTGACA TGGCTACAGT TGTTTGCAGC 300
 ATCTTAGGTG TTTGTCTTGT CATGATCCCA AACATTGTTG ATGAAGACAA TTCTTTGTTA 360

AATGCCTGGA AAGAAGCCTT TGGGTACACC ATGACTGTGA TGGCTGGACT GACCACTGCT 420
 CTCTCAATGA TAGTATACAG ATCCATCAAG GAGAAGATCA GCATGTGGAC TGCACTGTTT 480
 ACTTTTGGTT GGA CTGGGAC AATT TGGGGA ATATCTACTA TGTTTATTCT TCAAGAACCC 540
 ATCATCCCAT TAGATGGAGA AACCTGGAGT TATCTCATTG CTATATGTGT CTGTTCTACT 600
 GCAGCATTCT TAGGAGTTTA TTATGCCTTG GACAAATTCC ATCCAGCTTT GGT TAGCACA 660
 GTACAACATT TGGAGATTGT GGTAGCTATG GTCTTG CAGC TTCTCGTGCT GCACATATTT 720
 CCTAGCATCT ATGATGTTTT TGGAGGGGTA ATCATTATGA TTAGTGTTTT TGTCCTTGCT 780
 GGCTATAAAC TTTACTGGAG GAATTTAAGA AGGCAGGACT ACCAGGAAAT ATTAGACTCT 840
 CCCATTAAAT GAATACCTGA TTATTATTGT CTCATTAATG TTCAGTTATT AATATGTATA 900
 CTGCCATTTT AATGTTTACC TATGAATGTC TTTTGTGTTA TATAACTGAC AGAGTGCTAT 960
 AAAATATATA ATATATACAA ATGCAGAAAA TTTATTCTAG TCTAATATAT TCAAATACAA 1020
 ATATTAAATA TATGAAATAC GTTAAAAAAA AAAAAAAAAA AAA 1063

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Trp Arg Ala Thr Thr Thr Val Phe Ser Ala Ile Leu Ala Phe Leu
 1 5 10 15
 Leu Val Asp Glu Lys Met Ala Tyr Val Asp Met Ala Thr Val Val Cys
 20 25 30
 Ser Ile Leu Gly Val Cys Leu Val Met Ile Pro Asn Ile Val Asp Glu
 35 40 45
 Asp Asn Ser Leu Leu Asn Ala Trp Lys Glu Ala Phe Gly Tyr Thr Met
 50 55 60
 Thr Val Met Ala Gly Leu Thr Thr Ala Leu Ser Met Ile Val Tyr Arg
 65 70 75 80
 Ser Ile Lys Glu Lys Ile Ser Met Trp Thr Ala Leu Phe Thr Phe Gly
 85 90 95
 Trp Thr Gly Thr Ile Trp Gly Ile Ser Thr Met Phe Ile Leu Gln Glu

| | | |
|---|-----|-----|
| 100 | 105 | 110 |
| Pro Ile Ile Pro Leu Asp Gly Glu Thr Trp Ser Tyr Leu Ile Ala Ile | | |
| 115 | 120 | 125 |
| Cys Val Cys Ser Thr Ala Ala Phe Leu Gly Val Tyr Tyr Ala Leu Asp | | |
| 130 | 135 | 140 |
| Lys Phe His Pro Ala Leu Val Ser Thr Val Gln His Leu Glu Ile Val | | |
| 145 | 150 | 155 |
| Val Ala Met Val Leu Gln Leu Leu Val Leu His Ile Phe Pro Ser Ile | | |
| 165 | 170 | 175 |
| Tyr Asp Val Phe Gly Gly Val Ile Ile Met Ile Ser Val Phe Val Leu | | |
| 180 | 185 | 190 |
| Ala Gly Tyr Lys Leu Tyr Trp Arg Asn Leu Arg Arg Gln Asp Tyr Gln | | |
| 195 | 200 | 205 |
| Glu Ile Leu Asp Ser Pro Ile Lys | | |
| 210 | 215 | |

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | |
|---|-----|
| TGGCCAAAGA GGCCTAGCCG GGAGCGGGCG AGGCGGCGGC GGCAGCAGCG ATGGCAGGAA | 60 |
| TAGAGTTGGA GCGGTGCCAG CAGCAGGCCA ACGAGGTGAC GGAAATTATG CGTAACAAC | 120 |
| TCGGCAAGGT CCTGGAGCGT GGTGTGAAGC TGGCCGAAC | 180 |
| GCAGCAGCGT TCAGACCAAC | |
| TCCTGGATAT GAGCTCAACC TTCAACAAGA CTACACAGAA CCTGGCCCAG AAGAAGTGCT | 240 |
| GGGAGAACAT CCGTTACCGG ATCTGCGTGG GGCTGGTGGT GGTGGTGTC CTGCTCATCA | 300 |
| TCCTGATTGT GCTGCTGGTC GTCTTTCTCC CTCAGAGCAG TGACAGCAGT AGTGCC | 356 |

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Gly Ile Glu Leu Glu Arg Cys Gln Gln Gln Ala Asn Glu Val
1 5 10 15
Thr Glu Ile Met Arg Asn Asn Phe Gly Lys Val Leu Glu Arg Gly Val
20 25 30
Lys Leu Ala Glu Leu Gln Gln Arg Ser Asp Gln Leu Leu Asp Met Ser
35 40 45
Ser Thr Phe Asn Lys Thr Thr Gln Asn Leu Ala Gln Lys Lys Cys Trp
50 55 60
Glu Asn Ile Arg Tyr Arg Ile Cys Val Gly Leu Val Val Val Gly Val
65 70 75 80
Leu Leu Ile Ile Leu Ile Val Leu Leu Val Val Phe Leu Pro Gln Ser
85 90 95
Ser Asp Ser Ser Ser Ala
100

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 60
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA 92

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

| | |
|---|------|
| GGGCCTCAAC TTTGGCGTCG TGAGATTCTT GTGAGGCGTC TGCCTGGAAG CCGGCAGCAA | 60 |
| TTTGTCTTCT TTAAAGAGAA AAAGAAGGCT AGGGACTCAG ATTCCTGGAT TCTGAGATCC | 120 |
| AGACCAGCTC CTCCCAGACC TCTCCAGAAG AAGCCATGGG AACCCTCGT ATCCAGCATT | 180 |
| TGCTGATCCT CCTGGTCCTA GGAGCCTCCC TCCTGACCTC GGGCCTAGAG CTGTATTGTC | 240 |
| AAAAGGGTCT GTCCATGACT GTGGAAGCAG ATCCAGCCAA TATGTTTAAC TGGACCACAG | 300 |
| AGGAAGTGGA GACTTGTGAC AAAGGGGCAC TTTGCCAGGA AACCATACTA ATAATTAAAG | 360 |
| CAGGGACTGA GACAGCCATT TTGGCCACGA AGGGCTGCAT CCCGGAAGGG GAGGAGGCCA | 420 |
| TAACAATTGT CCAGCACTCT TCACCTCCCG GCCTGATCGT GACCTCCTAC AGTAACTACT | 480 |
| GTGAGGATTC CTTCTGTAAT GACAAAGACA GCCTGTCTCA GTTTTGGGAG TTCAGTGAGA | 540 |
| CCACAGCTTC CACTGTGTCA ACAACCCTCC ATTGTCCAAC CTGTGTGGCT TTGGGGACCT | 600 |
| GTTTCAGTGC TCCTTCTCTT CCCTGTCCCA ATGGTACAAC TCGATGCTAT CAAGGAAAAC | 660 |
| TTGAGATCAC TGGAGGTGGC ATTGAGTCGT CTGTGGAGGT CAAAGGCTGT ACAGCCATGA | 720 |
| TTGGCTGCAG GCTGATGTCT GGAATCTTAG CAGTAGGACC CATGTTTGTG AGGGAAGCGT | 780 |
| GGCCACATCA GCTGCTCACT CAACCTCGAA AGACTGAAAA TGGGGCCACC TGTCTTCCCA | 840 |
| TTCTGTTTTG GGGGTTACAG CTA CTGCTGC CATTGCTGCT GCCATCATTT ATTCAC'TTTT | 900 |
| CCTAAGAAGG CACTTCTGGG CCTGGGTCTG AGGACATCTT TTTTGA CTGG GAGCCTTCTT | 960 |
| ACTGTTGAGG TTCAACAAGC TGAGGAGTAG ATGGGAATTT GAGGGAGAAT ACAGAGATAC | 1020 |
| TATGAACGTA TTTGACATTT TTAATACAAT TTCTGCTATA ATTTTGTAT GCAGTAGGCG | 1080 |
| TTACTAATAA ACATTTCTGC TGTGAAAAAA AAAAAAAAAA AAAAAAAAAA A | 1131 |

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Thr | Pro | Arg | Ile | Gln | His | Leu | Leu | Ile | Leu | Leu | Val | Leu | Gly |
| 1 | | | | | | | | 5 | | | 10 | | | 15 | |

Ala Ser Leu Leu Thr Ser Gly Leu Glu Leu Tyr Cys Gln Lys Gly Leu
20 25 30

Ser Met Thr Val Glu Ala Asp Pro Ala Asn Met Phe Asn Trp Thr Thr
35 40 45

Glu Glu Val Glu Thr Cys Asp Lys Gly Ala Leu Cys Gln Glu Thr Ile
50 55 60

Leu Ile Ile Lys Ala Gly Thr Glu Thr Ala Ile Leu Ala Thr Lys Gly
65 70 75 80

Cys Ile Pro Glu Gly Glu Glu Ala Ile Thr Ile Val Gln His Ser Ser
85 90 95

Pro Pro Gly Leu Ile Val Thr Ser Tyr Ser Asn Tyr Cys Glu Asp Ser
100 105 110

Phe Cys Asn Asp Lys Asp Ser Leu Ser Gln Phe Trp Glu Phe Ser Glu
115 120 125

Thr Thr Ala Ser Thr Val Ser Thr Thr Leu His Cys Pro Thr Cys Val
130 135 140

Ala Leu Gly Thr Cys Phe Ser Ala Pro Ser Leu Pro Cys Pro Asn Gly
145 150 155 160

Thr Thr Arg Cys Tyr Gln Gly Lys Leu Glu Ile Thr Gly Gly Gly Ile
165 170 175

Glu Ser Ser Val Glu Val Lys Gly Cys Thr Ala Met Ile Gly Cys Arg
180 185 190

Leu Met Ser Gly Ile Leu Ala Val Gly Pro Met Phe Val Arg Glu Ala
195 200 205

Cys Pro His Gln Leu Leu Thr Gln Pro Arg Lys Thr Glu Asn Gly Ala
210 215 220

Thr Cys Leu Pro Ile Pro Val Trp Gly Leu Gln Leu Leu Leu Pro Leu
225 230 235 240

Leu Leu Pro Ser Phe Ile His Phe Ser
245

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | | | | | | |
|------------|-------------|------------|-------------|-------------|-------------|------|
| GCTCCGGGCC | GGCTGCGGAG | CGACTCCCCG | CCGCCAAGTG | GGCGGCGTGG | CTGTCGGGAA | 60 |
| AGAAGGGCTG | GGGCCTGCCG | TTCTTCCTCC | CGAGTATCCC | CTCCAGCTGG | ACGACCCAC | 120 |
| GCTGCAGCAC | GGGCTTCCGG | CTTCTCTCCT | CAGTGGCCAA | TTGAGGGCA | CAGCGGGCTC | 180 |
| CGGAGGCGCG | GCGGCAAGCC | TATCCCGCCT | CCCAACCACA | GCCTCCAGCA | CCCGAGAGAA | 240 |
| CGGCCGCCCA | CAGCACACGT | TCTCCGACA | GGAGGGCGAA | GGCCAAGAC | CTGGAGAGAT | 300 |
| GGTCAGCTCT | CAAAAAAGGC | ACAAACAATT | GAAGGATGGA | TACCATGGCA | TATGTTAAAA | 360 |
| GCGTGTGAA | AGGAAAATAA | GAAAGCCAGG | AATCTCAGGA | TGAATCAGTC | TAGATCGAGA | 420 |
| TCAGATGGTG | GCAGTGAAGA | AACCTTACCT | CAAGACCATA | ATCATCATGA | AAATGAGAGA | 480 |
| AGATGGCAGC | AAGAGCGTCT | CCACAGAGAA | GAGGCCTATT | ATCAGTTTAT | TAATGAACTC | 540 |
| AATGATGAAG | ATTATCGGCT | TATGAGAGAC | CATAATCTTT | TAGGCACCCC | TGGAGAAATA | 600 |
| ACATCAGAAG | AACTGCAACA | GCGGTTAGAT | GGCGTCAAGG | AACAAC TAGC | ATCTCAGCCT | 660 |
| GACTTGAGAG | ATGGAACGAA | TTACAGAGAC | TCAGAAGTCC | CTAGAGAAAG | TTACATGAA | 720 |
| GATTCTCTTC | TAGAATGGTT | GAACACCTTT | CGGCGCACAG | GAAATGCAAC | TCGAAGTGGA | 780 |
| CAAAATGGGA | ACCAAAC TTG | GAGAGCTGTG | AGTCGAACAA | ACCCGAACAA | TGGAGAGTTT | 840 |
| CGGTTTAGTT | TGGAAATCCA | CGTAAATCAT | GAAAATAGAG | GATTTGAAAT | TCATGGAGAA | 900 |
| GATTATACAG | ACATTCCACT | TTCAGATAGT | AACAGAGATC | ATACTGCAAA | TAGGCAACAA | 960 |
| AGGTCAACTA | GTCCTGTGGC | TAGGCGAACA | AGAAGCCAAA | CCTCAGTGAA | TTTCAATGGT | 1020 |
| AGTAGTTCCA | ACATTCCAAG | GACTAGGCTT | GCTTCAAGGG | GGCAAAATCC | AGCTGAAGGA | 1080 |
| TCTTTCTCAA | CATTGGGAAG | GTTAAGAAAT | GGAATTGGGG | GAGCAGCTGG | CATTCCTCGA | 1140 |
| GCTAACGCTT | CACGCACTAA | TTTCAGTAGT | CACACAAACC | AATCAGGTGG | TAGTGAAC TC | 1200 |
| AGGCAAAGGG | AGGGGCAACG | GTTTGGAGCA | GCACATGTTT | GGGAAAATGG | GGCTAGAAGT | 1260 |
| AATGTTACAG | TGAGGAATAC | AAACCAAAGA | TTAGAGCCAA | TAAGATTACG | ATCTACTTCC | 1320 |
| AATAGTCGAA | GCCGTTCAAC | AATTCAGAGA | CAGAGTGGCA | CTGTTTATCA | TAATTCCCAA | 1380 |
| AGGGAAAGTA | GACCAGTACA | GCAAACCACT | AGAAGATCTG | TTAGGAGGAG | AGGTAGAACT | 1440 |
| CGAGTCTTTT | TAGAGCAAGA | TAGAGAACGA | GAACGCAGAG | G TACTGCATA | TACCCCATTC | 1500 |
| TCTAATTCAA | GGCTTG TGTC | AAGAATAACA | G TAGAAGAAG | GAGAAGAATC | CAGCAGATCC | 1560 |
| TCAACTGCTG | TACGACGACA | TCCAACAATC | ACACTGGACC | TTCAAGTGAG | AAGGATCCGT | 1620 |

| | | | | | | |
|-------------|------------|------------|------------|-------------|------------|------|
| CCTGGAGAAA | ATAGAGATCG | GGATAGTATT | GCAAATAGAA | CTCGATCCAG | AGTAGGGCTA | 1680 |
| GCAGAAAATA | CAGTCACTAT | TGAAAGCAAT | AGTGGGGGCT | TTCGCCGAAC | CATTTCTCGT | 1740 |
| TTAGAGCGGT | CAGGTATTCG | AACCTATGTT | AGTACCATAA | CAGTTCCCCT | TCGTAGGATT | 1800 |
| TCTGAGAATG | AGCTTGTTGA | GCCATCATCA | GTGGCTCTTC | GGTCAATTTT | AAGGCAGATC | 1860 |
| ATGACTGGGT | TTGGAGAACT | GAGTTCCTTA | ATGGAGGCCG | ATTCTGAGTC | AGAACTTCAA | 1920 |
| AGAAATGGCC | AGCATTTACC | AGACATGCAC | TCAGAACTGA | GTAACCTTAGG | TACAGATAAC | 1980 |
| AACAGGAGCC | AGCACAGGGA | AGGTCCTCT | CAAGACAGGC | AGGCCCAAGG | AGACAGCACT | 2040 |
| GAAATGCATG | GTGAAAACGA | GACCACCCAG | CCTCATACTC | GAAACAGTGA | CAGTAGGGGT | 2100 |
| GGCAGGCAGT | TGCGAAATCC | AAACAATTTA | GTTGAAACTG | GAACACTACC | CATTCTTCGC | 2160 |
| CTTGCTCACT | TTTTTTTACT | AAATGAAAGT | GATGATGATG | ATCGAATACG | TGGTTTAACC | 2220 |
| AAAGAGCAGA | TTGACAATCT | TTCCACCAGG | CACTATGAGC | ATAACAGTAT | TGATAGTGAA | 2280 |
| CTAGGTAAAA | TCTGTAGTGT | TTGTATTAGT | GACTATGTAA | CTGGAAACAA | GCTCAGGCAA | 2340 |
| TTACCTTGCA | TGCATGAATT | TCACATTCAT | TGTATTGACC | GATGGCTCTC | AGAGAATTGC | 2400 |
| ACTTGTCCGA | TCTGTCGGCA | GCCTGTTTTA | GGGTCTAACA | TAGCAAACAA | TGGGTAAGGT | 2460 |
| GATGGGATCT | ACTCAAATAC | TGTTTTTTAG | TAGAACTGAA | TGTTCAAGCA | TTGTTTTGCT | 2520 |
| GAGTTATTTG | TGATTAGCTA | ACCAGGATGA | AAAATAACAG | ATTATATATA | GTTTGAACTA | 2580 |
| TTTTTCGTGT | GCTTTTTTAA | ACTTGTTAAA | AAGAAATTTA | TATAAAATTT | AAAATACAAA | 2640 |
| TGTTAAATTA | TCCAGAAATA | CAGAATAGTT | AATATTGCTA | GAACCAAATA | ACCTCTAAAA | 2700 |
| TGTTTTTATT | TTGGTAATTT | TGTCATGCTA | AGCACTTTTG | TATCTGCACA | ATTCAGTAGG | 2760 |
| TTAAGAATCA | ATCTTCTTTT | TCTTAATAGT | ACAGCAGACT | TTAGCTTCAA | GTTTCATAGG | 2820 |
| CTTAGTACTT | ATATCTAGAC | ATTTGTGTCT | AAATAAGCTT | TTCATTAACT | TTTTATTTTA | 2880 |
| AGGACAGTAT | CTTTTCATGA | AAGAGTATTT | GGCTGAATGT | TTGCTATATA | TATGTTACTT | 2940 |
| GAAATGTTAA | ATTTAATATG | CAGCATACCA | TAGGTGTATA | TATAGGTATA | TAATTTTAAG | 3000 |
| GTTAAAATAT | TCAGTCTAAC | AAGTTTGGTT | CTTATTTAAG | CTTTTGGGCT | AATACTGCAT | 3060 |
| ATGGCACAAAT | GTTTAATATT | GGCAAGTTCA | TCTCAGAGAA | AGGGGATTCA | GATATAATTT | 3120 |
| TAAAGTAGAG | ATAATTTACT | GAAGCGTCTC | TGACAATCTA | ACTTATTAGA | CAGCAAGCAA | 3180 |
| TATATAATAC | TGAAAAAGTA | TTCAGAAATG | GAAAATTTAC | ATCATATAGG | TTATTTAACT | 3240 |
| TGTGTTCAGC | CTTTTTGTAA | CTTTTTTGAA | AGTGCAAACA | ATTCTTTGGA | TTATTAAATA | 3300 |

AGGTATACAG TATGCATGGT TTCTCAAATT TAGCTTTAAA ATCTAAAAGT CTATAAAGAA 3360
 TCAGATGCAT AGGCAATATG TTAAGTTCAC TTGGAGGCTA AAAATCTCCA GTGAAAACAA 3420
 AACGAAAACC TTTAAGAGAA TGTAGAGTTT ATATAAACAC AAAGTATGCA TTGAAGATCT 3480
 GTTTCTACCA ATAAACATTA AAACAAAAAA AAAAAAAAAA AAAAAAA 3527

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 685 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Asn Gln Ser Arg Ser Arg Ser Asp Gly Gly Ser Glu Glu Thr Leu
 1 5 10 15
 Pro Gln Asp His Asn His His Glu Asn Glu Arg Arg Trp Gln Gln Glu
 20 25 30
 Arg Leu His Arg Glu Glu Ala Tyr Tyr Gln Phe Ile Asn Glu Leu Asn
 35 40 45
 Asp Glu Asp Tyr Arg Leu Met Arg Asp His Asn Leu Leu Gly Thr Pro
 50 55 60
 Gly Glu Ile Thr Ser Glu Glu Leu Gln Gln Arg Leu Asp Gly Val Lys
 65 70 75 80
 Glu Gln Leu Ala Ser Gln Pro Asp Leu Arg Asp Gly Thr Asn Tyr Arg
 85 90 95
 Asp Ser Glu Val Pro Arg Glu Ser Ser His Glu Asp Ser Leu Leu Glu
 100 105 110
 Trp Leu Asn Thr Phe Arg Arg Thr Gly Asn Ala Thr Arg Ser Gly Gln
 115 120 125
 Asn Gly Asn Gln Thr Trp Arg Ala Val Ser Arg Thr Asn Pro Asn Asn
 130 135 140
 Gly Glu Phe Arg Phe Ser Leu Glu Ile His Val Asn His Glu Asn Arg
 145 150 155 160
 Gly Phe Glu Ile His Gly Glu Asp Tyr Thr Asp Ile Pro Leu Ser Asp
 165 170 175
 Ser Asn Arg Asp His Thr Ala Asn Arg Gln Gln Arg Ser Thr Ser Pro
 180 185 190

Val Ala Arg Arg Thr Arg Ser Gln Thr Ser Val Asn Phe Asn Gly Ser
195 200 205

Ser Ser Asn Ile Pro Arg Thr Arg Leu Ala Ser Arg Gly Gln Asn Pro
210 215 220

Ala Glu Gly Ser Phe Ser Thr Leu Gly Arg Leu Arg Asn Gly Ile Gly
225 230 235 240

Gly Ala Ala Gly Ile Pro Arg Ala Asn Ala Ser Arg Thr Asn Phe Ser
245 250 255

Ser His Thr Asn Gln Ser Gly Gly Ser Glu Leu Arg Gln Arg Glu Gly
260 265 270

Gln Arg Phe Gly Ala Ala His Val Trp Glu Asn Gly Ala Arg Ser Asn
275 280 285

Val Thr Val Arg Asn Thr Asn Gln Arg Leu Glu Pro Ile Arg Leu Arg
290 295 300

Ser Thr Ser Asn Ser Arg Ser Arg Ser Pro Ile Gln Arg Gln Ser Gly
305 310 315 320

Thr Val Tyr His Asn Ser Gln Arg Glu Ser Arg Pro Val Gln Gln Thr
325 330 335

Thr Arg Arg Ser Val Arg Arg Arg Gly Arg Thr Arg Val Phe Leu Glu
340 345 350

Gln Asp Arg Glu Arg Glu Arg Arg Gly Thr Ala Tyr Thr Pro Phe Ser
355 360 365

Asn Ser Arg Leu Val Ser Arg Ile Thr Val Glu Glu Gly Glu Glu Ser
370 375 380

Ser Arg Ser Ser Thr Ala Val Arg Arg His Pro Thr Ile Thr Leu Asp
385 390 395 400

Leu Gln Val Arg Arg Ile Arg Pro Gly Glu Asn Arg Asp Arg Asp Ser
405 410 415

Ile Ala Asn Arg Thr Arg Ser Arg Val Gly Leu Ala Glu Asn Thr Val
420 425 430

Thr Ile Glu Ser Asn Ser Gly Gly Phe Arg Arg Thr Ile Ser Arg Leu
435 440 445

Glu Arg Ser Gly Ile Arg Thr Tyr Val Ser Thr Ile Thr Val Pro Leu
450 455 460

Arg Arg Ile Ser Glu Asn Glu Leu Val Glu Pro Ser Ser Val Ala Leu
465 470 475 480

Arg Ser Ile Leu Arg Gln Ile Met Thr Gly Phe Gly Glu Leu Ser Ser
485 490 495

Leu Met Glu Ala Asp Ser Glu Ser Glu Leu Gln Arg Asn Gly Gln His
500 505 510

Leu Pro Asp Met His Ser Glu Leu Ser Asn Leu Gly Thr Asp Asn Asn
515 520 525

Arg Ser Gln His Arg Glu Gly Ser Ser Gln Asp Arg Gln Ala Gln Gly
530 535 540

Asp Ser Thr Glu Met His Gly Glu Asn Glu Thr Thr Gln Pro His Thr
545 550 555 560

Arg Asn Ser Asp Ser Arg Gly Gly Arg Gln Leu Arg Asn Pro Asn Asn
565 570 575

Leu Val Glu Thr Gly Thr Leu Pro Ile Leu Arg Leu Ala His Phe Phe
580 585 590

Leu Leu Asn Glu Ser Asp Asp Asp Arg Ile Arg Gly Leu Thr Lys
595 600 605

Glu Gln Ile Asp Asn Leu Ser Thr Arg His Tyr Glu His Asn Ser Ile
610 615 620

Asp Ser Glu Leu Gly Lys Ile Cys Ser Val Cys Ile Ser Asp Tyr Val
625 630 635 640

Thr Gly Asn Lys Leu Arg Gln Leu Pro Cys Met His Glu Phe His Ile
645 650 655

His Cys Ile Asp Arg Trp Leu Ser Glu Asn Cys Thr Cys Pro Ile Cys
660 665 670

Arg Gln Pro Val Leu Gly Ser Asn Ile Ala Asn Asn Gly
675 680 685

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

| | |
|---|-----|
| CAGCCTGGGC TCCGCGCAGC CCACCGATCT GGGCGCCCAC AAGCGGCCGG CATCCGTGTC | 60 |
| GAGCAGCGCT GCCGTGGAGC ACGAGCAGCG TGAGGCGGCA GCCAAGGAGA AACAAACGCC | 120 |
| GCCGCCTGCG CACCGGGGCC CGGCCGACAG CCTGTCCACC GCGGCCGGGG CCGCCGAGCT | 180 |

| | |
|---|------|
| GAGCGCGGAA GGTGCGGGCA AGAGCCGCGG GTCTGGAGAG CAGGACTGGG TCAACAGGCC | 240 |
| CAAGACCGTG CGCGACACGC TGCTGGCGCT GCACCAGCAC GGCCACTCGG GGCCCTTCGA | 300 |
| GAGCAAGTTT AAGAAGGAGC CGGCCCTGAC TGCAGGCAGG TTGTTGGGTT TCGAGGCCAA | 360 |
| CGGGGCCAAC GGGTCTAAAG CAGTTGCAAG AACAGCAAGG AAAAGGAAGC CCTCTCCAGA | 420 |
| ACCAGAAGGT GAAGTCGGGC CCCCTAAGAT CAACGGAGAG GCCCAGCCGT GGCTGTCCAC | 480 |
| ATCCACAGAG GGGCTCAAGA TCCCCATGAC TCCTACATCC TCTTTTGTGT CTCCGCCACC | 540 |
| ACCCACTGCC TCACCTCAT TCCAACCGGAC CACACCGCCT GAAGCGGCC AGAATGGCCA | 600 |
| GTCCCCCATG GCAGCCCTGA TCTTAGTAGC AGACAATGCA GGGGGCAGTC ATGCCTCAAA | 660 |
| AGATGCCAAC CAGGTTCACT CCACTACCAG GAGGAATAGC AACAGTCCGC CCTCTCCGTC | 720 |
| CTCTATGAAC CAAAGAAGGC TGGGCCCCAG AGAGGTGGGG GGCCAGGGAG CAGGCAACAC | 780 |
| AGGAGGACTG GAGCCAGTGC ACCCTGCCAG CCTCCCGGAC TCCTCTCTGG CAACCAGTGC | 840 |
| CCCCTGTGTC TGCACCTCT GCCACGAGCG GCTGGAGGAC ACCCATTTTG TGCAGTGCCC | 900 |
| GTCCGTCCCT TCGCACAAGT TCTGCTTCCC TTGCTCCAGA CAAAGCATCA AACAGCAGGG | 960 |
| AGCTAGTGGA GAGGTCTATT GTCCCAGTGG GGAAAAATGC CCTCTTGTGG GCTCCAATGT | 1020 |
| CCCCTGGGCC TTTATGCAAG GGGAAATTGC AACCATCCTT GCTGGAGATG TGAAAGTGAA | 1080 |
| AAAAGAGAGA GACTCGTGAC TTTTCCGGTT TCAGAAAAAC CCAATGATTA CCCTTAATTA | 1140 |
| AAACTGCTTG AATTGTATAT ATATCTCCAT ATATATATAT ATCCAAGACA AGGGAAATGT | 1200 |
| AGACTTCATA AACATGGCTG TATAATTTTG ATTTTTTTGT AATACATTGT GTTTCTATAT | 1260 |
| TTTTTTTGAC GACAAAAGGT ATGTACTTAT AAAGACATTT TTTTCTTTTG TTAACGTTAT | 1320 |
| TAGCATATCT TTGTGCTTTA TTATCCTGGT GACAGTTACC GTTCTATGTA GGCTGTGACT | 1380 |
| TGCGCTGCTT TTTTAGAGCA CTTGGCAAAT CAGAAATGCT TCTAGCTGTA TTTGTATGCA | 1440 |
| CTTATTTTAA AAAAAAAAAA AAA | 1463 |

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Pro | Thr | Ser | Ser | Phe | Val | Ser | Pro | Pro | Pro | Pro | Thr | Ala | Ser | 1 | 5 | 10 | 15 |
| Pro | His | Ser | Asn | Arg | Thr | Thr | Pro | Pro | Glu | Ala | Ala | Gln | Asn | Gly | Gln | 20 | 25 | 30 | |
| Ser | Pro | Met | Ala | Ala | Leu | Ile | Leu | Val | Ala | Asp | Asn | Ala | Gly | Gly | Ser | 35 | 40 | 45 | |
| His | Ala | Ser | Lys | Asp | Ala | Asn | Gln | Val | His | Ser | Thr | Thr | Arg | Arg | Asn | 50 | 55 | 60 | |
| Ser | Asn | Ser | Pro | Pro | Ser | Pro | Ser | Ser | Met | Asn | Gln | Arg | Arg | Leu | Gly | 65 | 70 | 75 | 80 |
| Pro | Arg | Glu | Val | Gly | Gly | Gln | Gly | Ala | Gly | Asn | Thr | Gly | Gly | Leu | Glu | 85 | 90 | 95 | |
| Pro | Val | His | Pro | Ala | Ser | Leu | Pro | Asp | Ser | Ser | Leu | Ala | Thr | Ser | Ala | 100 | 105 | 110 | |
| Pro | Leu | Cys | Cys | Thr | Leu | Cys | His | Glu | Arg | Leu | Glu | Asp | Thr | His | Phe | 115 | 120 | 125 | |
| Val | Gln | Cys | Pro | Ser | Val | Pro | Ser | His | Lys | Phe | Cys | Phe | Pro | Cys | Ser | 130 | 135 | 140 | |
| Arg | Gln | Ser | Ile | Lys | Gln | Gln | Gly | Ala | Ser | Gly | Glu | Val | Tyr | Cys | Pro | 145 | 150 | 155 | 160 |
| Ser | Gly | Glu | Lys | Cys | Pro | Leu | Val | Gly | Ser | Asn | Val | Pro | Trp | Ala | Phe | 165 | 170 | 175 | |
| Met | Gln | Gly | Glu | Ile | Ala | Thr | Ile | Leu | Ala | Gly | Asp | Val | Lys | Val | Lys | 180 | 185 | 190 | |
| Lys | Glu | Arg | Asp | Ser | | | | | | | | | | | | 195 | | | |

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| CATTTTCTG | GTCCTTCTTA | AAAGTAATCA | CTCTTAAATT | TTGTGCTTAT | TCTGTTGTTT | 60 |
| TAAAAAATAG | TTTAAACAAA | TATGTGTGTA | CTCATAAACA | TAGGTACTT | TTGCTTCTTT | 120 |
| TTGAGATATA | TTTAAATTTT | ATTGTGGTCT | ACATATTCTT | CAGCAGTTTG | TTTTTTTACC | 180 |
| CAATATTATG | TTTCATCTGT | ATTACTGCAT | TTACTATCCC | TAGTTGATTC | ACTTCCCTGA | 240 |
| AGTACAATAT | TCAGTTGTGT | GGCTATACCA | TAATTTAGTT | ATTCATTTTG | TTGTCAGTAA | 300 |
| AATTTGGGTG | ATTATCAGAT | TTTTTTCTAG | CATGAAAAAT | GCTACTARGA | ACATTCSTGT | 360 |
| ATGTGTCTAA | TGGTATACAC | TTTCAAGTGT | TTTTTTATAT | ATGTGAGAGT | AGATTACTTG | 420 |
| GACCTTGAAG | ATGAACATGC | TATCTTTTCC | AGATACTGCC | AATTATTTCA | GCAAGATATG | 480 |
| AGTTCCCATC | ATTTTATATT | TGTCAGCATT | TGATATTTCC | AGGCCTAGTG | ATTTCCAGTC | 540 |
| ATTTACTGGA | TATAATATGA | TTATCTCTGT | AGGGAGTTGA | TTCCATCTC | CTCAATTACT | 600 |
| AATAAAGTTA | AAAATCTTTT | CATATGTTTT | ATTGCCATTT | TTATTTCTTC | TGTAAAGTAC | 660 |
| CTACTCATGG | CTTTTTCTCA | TTTTTTGTTT | GTCATCATTG | AATTATAGGA | GTTTTGAGAG | 720 |
| AGTGAGCAAG | CTAGTCTGTG | TGTGTGTGTG | TGTGCGTGTG | TGTGTATCTC | CTTAATGTGT | 780 |
| TATATGTGAT | TGGAACTTCT | TCTCCACCT | TGATGCTTCC | TTTCTTCCCC | ACTTGTTTTA | 840 |
| GGTATCTTCT | GATGAAGTGG | AGTTATTTAT | GGTATGTTCT | CAGGAGCTAC | AATTTTTAAT | 900 |
| TTCAATATAA | TCAGTGTTTT | TAATTATCTT | ATGTTTAGCT | CTTTTGGGTC | ATGCTTAGGA | 960 |
| AATTCCTTCT | AAATTTTATT | GATAACAGTC | TTCCATACTT | TCTTCTAAAG | TCTTATATTT | 1020 |
| TGGCCTTTCA | TATTTATTCC | TTTAATCCAM | CTGGAGTAGA | TTTTTTTTTT | CCCTCTGTAG | 1080 |
| AGTTTGGAGT | AGAGATTTTA | TTTCCTTTTT | TTTTTTTTTT | TTTTTTTCTT | TTTTTTTGAG | 1140 |
| ACAGAGTCTT | GCTCTGTCGC | CCAGGCTGGA | GTGCAGTGGC | ACTATCTCAG | CTCACTGCAA | 1200 |
| CCTCCACCTC | CTGGGTTCAG | GCGATTCTCC | TGCCTCCGCC | TCCCGAGTAG | CTGGGACTAC | 1260 |
| AGGCATGTGC | CACCACGCCC | AGCTAATTTT | TTGTATTTTT | TTTAGTAGAG | ATGGGGTTCC | 1320 |
| ACCATGTTAG | CTAGGATGAT | TTGATTTTCC | TGACCTTGTG | ATCCGCCCCG | CTCGGCCTCC | 1380 |
| CAAAATGCTG | GGATTATAGG | TGTGAGCCAC | CACGTGGCCT | CATTTTATTC | TTTCATGTGG | 1440 |
| ATAGGCAGTT | GTTCCAGAAG | TATATAGTGA | GGAGCTTCTT | CTTTCTCTAA | TGATCTGCAA | 1500 |
| TGTCACCTTC | ATCATTTATG | AAGGTTGCAC | ATATACATGG | GAATTTTTTA | GTCTGGCATT | 1560 |
| AAATGTTCTT | CAAAAGAGTT | CCTGCAAACG | TTTTTGTTTT | TATTTCTTAC | TGTTCCCTTC | 1620 |
| ACGTACTCTC | TACTGAACTA | AACTCTGTAA | TGTGTCTCGA | AACTGTCCCA | CAATTTTCCT | 1680 |

TGTCTTAAGA GTTTAATGCT TTCATACACC TCTCACATTC AGCCTTGTGC TATTGTCTTA 1740
 GGTATATTTA TTTCTCTTTT GCTCCCAATT ATGTTGTAAA CTTTGTGAAG CAGGAAGGAT 1800
 ATATTGTTCA TCTTTGGTAG CATTAAACAA TGAATACAGT GTTTTTTACT TAATAGATAT 1860
 TTGGTAAATC ATTGAACTAA ATTGGGGTTT GGAATTGAAG GTCTTAGAAA TTACCTGACC 1920
 ACTCCCATTA TATTTGCCCA TCCATGATCA CTGAGATTTA TAGAGATTAG ATGCAATGCC 1980
 CAGTTTCACA TATGTTTTTG CATCACTGTC TCTTTTTTTC TTGAGCTTAT TCCAGAGTGT 2040
 CTTTAAATAT CCATTCCATG ATCAAATGGC TGAACATTA AAATGCTGTC CAGAAGTGTA 2100
 AAGCAATATG AAGATGCTAG AAAAGTTGAA GAGACACATA TATGGTAGGT CCAAGACCAT 2160
 TACACTTACT GAGTCCATTA CTAAAAATGA TGTTCACCTA ACATCAAAAC ACTCAGGATT 2220
 ACCCAAGCAC AATATACTGA TTTGCACCTC TGCCTTTGTT CATGCCCTT GTTCAGGAGA 2280
 ACTGCTTTCA TGTGCTACTG TCCATAGATC TTCTCTATCC TTACAGATTA ATTTCTTCCT 2340
 TTTGAATGCT ATGTTTCCAT ACTTTGACAT TCCTTCTGCA CCATTCAGAC CATATTTTAG 2400
 TTCTTTTTTA TGGTATCTCT CACTTTTGAT TGTCACCCCT TAAGTCAAAG ACAATTTTTT 2460
 CATCTGTGTC TTCTCAACAC CCAGCACAGG GCTATGTTTG GTAAAAATTA GGTATCCAAG 2520
 ATGTACTAAA TGAAAAAAAA AAAAAAA 2547

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Phe Phe Lys Arg Val Pro Ala Asn Val Phe Val Phe Ile Ser Tyr
 1 5 10 15
 Cys Ser Leu His Val Leu Ser Thr Glu Leu Asn Ser Val Met Cys Leu
 20 25 30
 Glu Thr Val Pro Gln Phe Ser Leu Ser
 35 40

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

| | |
|--|------|
| GCTCAACGGC CTCTTCTGGT TGCTGTCTTC CTCGTCCCTC CGGCCCTTCT TCCTACTCAG | 60 |
| CGTCTCACTT TTGGCCTATT TTCTGCTGGA TCTCTGGCAG CCTCGCTTTC TCCCTGACGT | 120 |
| TTCAGCATCA TCCCCAGAGG AGCCACACTC TGACAGTGAG GGTGCGGGGT CAGGCGCCCCG | 180 |
| GCCGCACCTG CTGAGTGTGC CCGAGTTGTG CAGATACCTG GCTGAGAGCT GGCTCACCTT | 240 |
| CCAGATTCAC CTGCAGGAGC TGCTGCAGTA CAAGAGGCAG AATCCAGCTC AGTTCTGCGT | 300 |
| TCGARTCTGC TCTGGCTGTG CTGTGTTGGC TGTGTTGGGA CACTATGTTT CAGGGATTAT | 360 |
| GATTTCTTAC ATTGTCTTGT TGAGTATCCT GCTGTGGCCC CTGGTGGTTT ATCATGARCT | 420 |
| GATCCAGAGG ATGTWCACTC GCCTGGAGCC CCTGCTCATG CAGCTGGACT ACAGCATGAA | 480 |
| GGCAGAAKCC AATGCCCTGC ATCACAACA CGACAAGAGG AAGCGTCAGG GGAAGAATGC | 540 |
| ACCCCCAGGA GGTGATGAGC CACTGGCAGA GACAGAGAGT GAAAGCGAGG CAGAGCTGGC | 600 |
| TGGCTTCTCC CCAGTGGTGG ATGTGAAGAA AACAGCATTG GCCTTGGCCA TTACAGACTC | 660 |
| AGAGCTGTCA GATGAGGAGG CTTCTATCTT GGAGAGTGGT GGCTTCTCCG TATCCCGGGC | 720 |
| CACAACTCCG CAGCTGACTG ATGTCTCCGA GGATTGAGC CAGCAGAGCC TGCCAAGTGA | 780 |
| ACCAGAGGAG ACCCTAAGCC GGGACCTAGG GGAGGGAGAG GAGGGAGAGC TGGCCCCCTCC | 840 |
| CGAAGACCTA CTAGGCCGTC CTCAAGCTCT GTCAAGGCAA GCCCTGGACT TGGAGGAAGA | 900 |
| GGAAGAGGAT GTGGCAGCTA AGGAAACCTT GTTGC GGCTC TCATCCCCC TCCACTTTGT | 960 |
| GAACACGCAC TTCAATGGGG CAGGGTCCCC CCCAGATGGA GTGAAATGCT CCCCTGGAGG | 1020 |
| ACCAGTGGAG AACTGAGCC CCGAGACAGT GAGTGGTGGC CTCACTGCTC TGCCCGGCAC | 1080 |
| CCTGTCACCT CCACTTTGCC TTGTTGGAAG TGACCCAGCC CCCTCCCCTT CCATTCTCCC | 1140 |
| ACCTGTTCCC CAGGACTCAC CCCAGCCCCT GCCTGCCCCCT GAGGAAGAAG AGGCACTCAC | 1200 |
| CACTGAGGAC TTTGAGTTGC TGGATCAGGG GGAGCTGGAG CAGCTGAATG CAGAGCTGGG | 1260 |
| CTTGGAGCCA GAGACACCGC CAAAACCCCC TGATGCTCCA CCCCTGGGGC CCGACATCCA | 1320 |
| TTCTCTGGTA CAGTCAGACC AAGAAGCTCA GGCCGTGGCA GAGCCATGAG CCAGCCGTTG | 1380 |

AGGAAGGAGC TGCAGGCACA GTAGGGCTTC CTGGCTAGGA GTGTTGCTGT TTCCTCCTTT 1440
 GCCTACCACT CTGGGGTGGG GCAGTGTGTG GGGAAAGCTGG CTGTCGGATG GTAGCTATTC 1500
 CACCYTCTGC CTGCCTGCCT GCCTGCTGTC CTGGGCATGG TGCAGTACCT GTGCCTAGGA 1560
 TTGGTTTTAA ATTTGTAAAT AATTTTCCAT TTGGGTTAGT GGATGTGAAC AGGGCTAGGG 1620
 AAGTCCTTCC CACAGCCTGC GCTTGCCTCC CTGCCTCATC TCTATTCTCA TTCCACTATG 1680
 CCCCAGCCC TGGTGGTCTG GCCCTTTCTT TTTCTCCTA TCCTCAGGGA CCTGTGCTGC 1740
 TCTGCCCTCA TGTCCCACTT GGTTGTTTAG TTGAGGCACT TTATAATTTT TCTCTTGTCT 1800
 TGTGTTCCCTT TCTGCTTTAT TTCCCTGCTG TGTCCGTGTC TTAGCAGCTC AACCCCATCC 1860
 TTTGCCAGCT CCTCCTATCC CGTGGGCACT GGCCAAGCTT TAGGGAGGCT CCTGGTCTGG 1920
 GAAGTAAAGA GTAAACCTGG GGCAGTGGGT CAGGCCAGTA GTTACACTCT TAGGTCACTG 1980
 TAGTCTGTGT AACCTTCACT GCATCCTTGC CCCATTCAGC CCGGCCTTTC ATGATGCAGG 2040
 AGAGCAGGGA TCCCGCAGTA CATGGCGCCA GCACTGGAGT TGGTGAGCAT GTGCTCTYTY 2100
 TTGAGATTAG GAGCTTCCTT ACTGCTCCTC TGGGTGATCC AAGTGATAGT GGACCCCTA 2160
 CTAGGGTCAG GAAGTGGACA CTAACATCTG TGCAGGTGTT GACTTGAAAA ATAAAGTGTT 2220
 GATTGGCTAG AAAAAAAAAA AAAAA 2245

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Ile Ser Tyr Ile Val Leu Leu Ser Ile Leu Leu Trp Pro Leu Val
 1 5 10 15
 Val Tyr His Glu Leu Ile Gln Arg Met Xaa Thr Arg Leu Glu Pro Leu
 20 25 30
 Leu Met Gln Leu Asp Tyr Ser Met Lys Ala Glu Xaa Asn Ala Leu His
 35 40 45
 His Lys His Asp Lys Arg Lys Arg Gln Gly Lys Asn Ala Pro Pro Gly
 50 55 60
 Gly Asp Glu Pro Leu Ala Glu Thr Glu Ser Glu Ser Glu Ala Glu Leu
 65 70 75 80

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gly | Phe | Ser | Pro | Val | Val | Asp | Val | Lys | Lys | Thr | Ala | Leu | Ala | Leu | 85 | 90 | 95 | |
| Ala | Ile | Thr | Asp | Ser | Glu | Leu | Ser | Asp | Glu | Glu | Ala | Ser | Ile | Leu | Glu | 100 | 105 | 110 | |
| Ser | Gly | Gly | Phe | Ser | Val | Ser | Arg | Ala | Thr | Thr | Pro | Gln | Leu | Thr | Asp | 115 | 120 | 125 | |
| Val | Ser | Glu | Asp | Leu | Asp | Gln | Gln | Ser | Leu | Pro | Ser | Glu | Pro | Glu | Glu | 130 | 135 | 140 | |
| Thr | Leu | Ser | Arg | Asp | Leu | Gly | Glu | Gly | Glu | Gly | Glu | Leu | Ala | Pro | | 145 | 150 | 155 | 160 |
| Pro | Glu | Asp | Leu | Leu | Gly | Arg | Pro | Gln | Ala | Leu | Ser | Arg | Gln | Ala | Leu | 165 | 170 | 175 | |
| Asp | Leu | Glu | Glu | Glu | Glu | Glu | Asp | Val | Ala | Ala | Lys | Glu | Thr | Leu | Leu | 180 | 185 | 190 | |
| Arg | Leu | Ser | Ser | Pro | Leu | His | Phe | Val | Asn | Thr | His | Phe | Asn | Gly | Ala | 195 | 200 | 205 | |
| Gly | Ser | Pro | Pro | Asp | Gly | Val | Lys | Cys | Ser | Pro | Gly | Gly | Pro | Val | Glu | 210 | 215 | 220 | |
| Thr | Leu | Ser | Pro | Glu | Thr | Val | Ser | Gly | Gly | Leu | Thr | Ala | Leu | Pro | Gly | 225 | 230 | 235 | 240 |
| Thr | Leu | Ser | Pro | Pro | Leu | Cys | Leu | Val | Gly | Ser | Asp | Pro | Ala | Pro | Ser | 245 | 250 | 255 | |
| Pro | Ser | Ile | Leu | Pro | Pro | Val | Pro | Gln | Asp | Ser | Pro | Gln | Pro | Leu | Pro | 260 | 265 | 270 | |
| Ala | Pro | Glu | Glu | Glu | Glu | Ala | Leu | Thr | Thr | Glu | Asp | Phe | Glu | Leu | Leu | 275 | 280 | 285 | |
| Asp | Gln | Gly | Glu | Leu | Glu | Gln | Leu | Asn | Ala | Glu | Leu | Gly | Leu | Glu | Pro | 290 | 295 | 300 | |
| Glu | Thr | Pro | Pro | Lys | Pro | Pro | Asp | Ala | Pro | Pro | Leu | Gly | Pro | Asp | Ile | 305 | 310 | 315 | 320 |
| His | Ser | Leu | Val | Gln | Ser | Asp | Gln | Glu | Ala | Gln | Ala | Val | Ala | Glu | Pro | 325 | 330 | 335 | |

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1406 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTGTGGGAA GAGCTGAAGC AGGCGCTCTT GGCTCGGCGC GGCCCGCTGC AATCCGTGGA 60
GGAACGCGCC GCCGAGCCAC CATCATGCCT GGGCACTTAC AGGAAGGCTT CGGCTGCGTG 120
GTCACCAACC GATTTCGACCA GTTATTTGAC GACGAATCGG ACCCCTTCGA GGTGCTGAAG 180
GCAGCAGAGA ACAAGAAAAA AGAAGCCGGC GGGGGCGGCG TTGGGGGCCC TGGGGCCAAG 240
AGCGCAGCTC AGGCCGCGGC CCAGACCAAC TCCAACGCGG CAGGCAAACA GCTGCGCAAG 300
GAGTCCCAGA AAGACCGCAA GAACCCGCTG CCCCCAGCG TTGGCGTGTT TGACAAGAAA 360
GAGGAGACGC AGCCGCCCCG GCGCTTAAG AAAGAAGGAA TAAGACGAGT TGAAGAAGA 420
CCTGATCAAC AACTTCAGGG TGAAGGAAA ATAATTGATA GAAGACCAGA AAGGCGACCA 480
CCTCGTGAAC GAAGATTCTGA AAAGCCACTT GAAGAAAAGG GTGAAGGAGG CGAATTTTCA 540
GTTGATAGAC CGATTATTGA CCGACCTATT CGAGGTCGTG GTGGTCTTGG AAGAGGTCGA 600
GGGGGCCGTG GACGTGGAAT GGGCCGAGGA GATGGATTG ATTCTCGTGG CAAACGTGAA 660
TTTGATAGGC ATAGTGGAAG TGATAGATCT TCTTTTTCAC ATTACAGTGG CCTGAAGCAC 720
GAGGACAAAC GTGGAGGTAG CGGATCTCAC AACTGGGGAA CTGTCAAAGA CGAATTAACT 780
GACTTGATC AATCAAATGT GACTGAGGAA ACACCTGAAG GTGAAGAACA TCATCCAGTG 840
GCAGACACTG AAAATAAGGA GAATGAAGTT GAAGAGGTAA AAGAGGAGGG TCCAAAAGAG 900
ATGACTTTGG ATGAGTGGA GGCTATTCAA AATAAGGACC GGGCAAAGT AGAATTTAAT 960
ATCCGAAAAC CAAATGAAGG TGCTGATGGG CAGTGGAAGA AGGGATTTGT TCTTCATAAA 1020
TCAAAGAGTG AAGAGGCTCA TGCTGAAGAT TCGGTTATGG ACCATCATTT CCGGAAGCCA 1080
GCAAATGATA TAACGTTTCA GCTGGAGATC AATTTTGGAG ACCTTGCCCG CCCAGGACGT 1140
GGCGGCAGGG GAGGACGAGG TGGACGTGGG CGTGGTGGGC GCCCAAACCG TGGCAGCAGG 1200
ACCGACAAGT CAAGTGCTTT TGCTCCTGAT GTGGATGACC CAGAGGCATT CCCAGTTTTG 1260
GCTTAAMTGG ATGCCATAAG ACAACCCTGG TTCCTTTGTG AACCTTTTGT TTCAAAGCTT 1320
TTGCATGCTT AAGGATTCCA AACGACTAAG AAATTAAAAA AAAAAAAAAA AAAAAAAAAA 1380
AAAAAAAAA AAAAAAAAAA AAAAAA 1406

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Gly | His | Leu | Gln | Glu | Gly | Phe | Gly | Cys | Val | Val | Thr | Asn | Arg | 1 | 5 | 10 | 15 |
| Phe | Asp | Gln | Leu | Phe | Asp | Asp | Glu | Ser | Asp | Pro | Phe | Glu | Val | Leu | Lys | 20 | 25 | 30 | |
| Ala | Ala | Glu | Asn | Lys | Lys | Lys | Glu | Ala | Gly | Gly | Gly | Gly | Val | Gly | Gly | 35 | 40 | 45 | |
| Pro | Gly | Ala | Lys | Ser | Ala | Ala | Gln | Ala | Ala | Ala | Gln | Thr | Asn | Ser | Asn | 50 | 55 | 60 | |
| Ala | Ala | Gly | Lys | Gln | Leu | Arg | Lys | Glu | Ser | Gln | Lys | Asp | Arg | Lys | Asn | 65 | 70 | 75 | 80 |
| Pro | Leu | Pro | Pro | Ser | Val | Gly | Val | Val | Asp | Lys | Lys | Glu | Glu | Thr | Gln | 85 | 90 | 95 | |
| Pro | Pro | Val | Ala | Leu | Lys | Lys | Glu | Gly | Ile | Arg | Arg | Val | Gly | Arg | Arg | 100 | 105 | 110 | |
| Pro | Asp | Gln | Gln | Leu | Gln | Gly | Glu | Gly | Lys | Ile | Ile | Asp | Arg | Arg | Pro | 115 | 120 | 125 | |
| Glu | Arg | Arg | Pro | Pro | Arg | Glu | Arg | Arg | Phe | Glu | Lys | Pro | Leu | Glu | Glu | 130 | 135 | 140 | |
| Lys | Gly | Glu | Gly | Gly | Glu | Phe | Ser | Val | Asp | Arg | Pro | Ile | Ile | Asp | Arg | 145 | 150 | 155 | 160 |
| Pro | Ile | Arg | Gly | Arg | Gly | Gly | Leu | Gly | Arg | Gly | Arg | Gly | Gly | Arg | Gly | 165 | 170 | 175 | |
| Arg | Gly | Met | Gly | Arg | Gly | Asp | Gly | Phe | Asp | Ser | Arg | Gly | Lys | Arg | Glu | 180 | 185 | 190 | |
| Phe | Asp | Arg | His | Ser | Gly | Ser | Asp | Arg | Ser | Ser | Phe | Ser | His | Tyr | Ser | 195 | 200 | 205 | |
| Gly | Leu | Lys | His | Glu | Asp | Lys | Arg | Gly | Gly | Ser | Gly | Ser | His | Asn | Trp | 210 | 215 | 220 | |
| Gly | Thr | Val | Lys | Asp | Glu | Leu | Thr | Asp | Leu | Asp | Gln | Ser | Asn | Val | Thr | 225 | 230 | 235 | 240 |

Glu Glu Thr Pro Glu Gly Glu Glu His His Pro Val Ala Asp Thr Glu
245 250 255

Asn Lys Glu Asn Glu Val Glu Glu Val Lys Glu Glu Gly Pro Lys Glu
260 265 270

Met Thr Leu Asp Glu Trp Lys Ala Ile Gln Asn Lys Asp Arg Ala Lys
275 280 285

Val Glu Phe Asn Ile Arg Lys Pro Asn Glu Gly Ala Asp Gly Gln Trp
290 295 300

Lys Lys Gly Phe Val Leu His Lys Ser Lys Ser Glu Glu Ala His Ala
305 310 315 320

Glu Asp Ser Val Met Asp His His Phe Arg Lys Pro Ala Asn Asp Ile
325 330 335

Thr Phe Gln Leu Glu Ile Asn Phe Gly Asp Leu Gly Arg Pro Gly Arg
340 345 350

Gly Gly Arg Gly Gly Arg Gly Gly Arg Gly Arg Gly Gly Arg Pro Asn
355 360 365

Arg Gly Ser Arg Thr Asp Lys Ser Ser Ala Phe Ala Pro Asp Val Asp
370 375 380

Asp Pro Glu Ala Phe Pro Val Leu Ala
385 390

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCGGACGCGG CCAGTCAGGT GCTCCTGGGC TCCGGTCTCA CCATCCTGTC CCAGCCGCTC 60

ATGTACGTGA AAGTGCTCAT CCAGGTGGGA TATGAGCCTC TTCCTCCAAC AATAGGACGA 120

AATATTTTGT GCGGCAAGT GTGTCAGCTT CCTGGTCTCT TTAGTTATGC TCAGCACATT 180

GCCAGTATCG ATGGGAGGCG CGGGTTGTTC ACAGGCTTAA CTCCAAGACT GTGTTCCGGA 240

GTCCTTGGA CTGTGGTCCA TGGTAAAGTT TTACAGCATT ACCAGGAGAG TGACAAGGGT 300

GAGGAGTTAG GAMCTGAAA TGTACARAAA GAAGTCTCAT CTCCTTTGA MCACGTTATC 360

AAGGAGACAA CTCGAGAGAT GATCGCTCGT TCTGCTGCTA CCCTCATCAC ACATCCCTTC 420
 CATGTTGATC ACTCTGAGAT CTATGGTACA RTTCATTGGC AGAGAATCCA AGTACTGTGG 480
 ACTTTGTGAT TCCATAATAA CCATCTATCG GGAAGAGGGC ATTCTAGGAT TTTTCGCGGG 540
 TCTTGTTTCT CGCCTTCTAG GTGACATCCT TTCTTTGTGG CTGTGTAAC TACTGGCCTA 600
 CCTCGTCAAT ACCTATGCAC TGGACAGTGG GGTTCCTACC ATGAATGAAA TGAAGAGTTA 660
 TTCTCAAGCT GTCACAGGAT TTTTGTGCGAG TATGTTGACC TATCCCTTTG TGCTTGTCTC 720
 CAATCTTATG GCTGTCAACA ACTGTGGTCT TGCTGGTGGA TGCCCTCCTT ACTCCCAAT 780
 ATATACGTCT TGGATAGACT GTTGGTGCAT GCTACAAAAA GAGGGGAATA TGAGCCGAGG 840
 AAATAGCTTA TTTTCCGGA AGGTCCCCTT TGGGAAGACT TATTGTTGTG ACCTGAAAAT 900
 GTTAATTTGA AGATGTGGGG CAGGGACAGT GACATTTCTG TAGTCCCAGA TGCACAGAAT 960
 TATGGGAGAG AATGTTGATT TCTATACAGT GTGGCGCGCT TTTTAAATAA TCATTTAATC 1020
 TTGGGAAAAT TCAGGTGTTT GGTGTCTGCC TTTTGTGTTT TTTTCCAG CACAACATAA 1080
 CTTACCACTG ATACTCCCC TTTAGTTATT CTGAATTAGG ATATTTTGC TCCAAATTCT 1140
 TATTTTACTT AACCAGAAGG GAAAAAAGT TGTATTTTCC TGAAGCTACA GGCACCTTGT 1200
 CATGTGATTT TTGAGTCTCA ATTTAAGGCT TTGTAAAATG AAGAGTAGAA TTCCAAGAAA 1260
 AATGAGAAAT AATTTTGTA AACTTAACAA AATCACTAAA TTAACTATA TGGGAGGTTA 1320
 TGAATTACTT TTTCTGGGT AGACCCTAAA ATGTCAGTAG CATGCACCAG AATCTGACTC 1380
 CCATTATGCT TCTAAGCACA TTTCATTGAC CTTGTCTCTC ATACTTCAAG AAAAGGACAG 1440
 TACATTGCTA CATTACCCTA GAAAGTCTGT GTGAGGATCT GCCCTTCAG TCTGTTATTG 1500
 CAAAGTAATA AAATGTCACC TACAGGGAGC CTCTGAGCCT ACTCTAGTTC AAGAGGCTAC 1560
 CTGAAAAAAA ATAAATAAGA TAAAGGGTCA GCAACAACAA AGAAAAAGAC AATTACAGAA 1620
 AATAAGCAAG ATTTGGAAAG GAAGTATAAT GGCACTTTTT TCCTCAAAGG AAGTTCTTGT 1680
 TTTCACATAA AATATGAAAA GCAGATCCTG CAGGAGTAAC CCCCTTCTTT AAGAGCCAAG 1740
 TATTTGCCAG TGCTTAAATT ACACCATAAC GTTCTAATTA TATATAATCT TTTGTTCTTC 1800
 AGTTTTTTGT TTTGTTTCTT TTTTGTATT GTTGCCGAAG GTGAGTAGTT TTGCATTTCT 1860
 GATGACAGCC TTGGAAAGTA TATTTGTAAC TCCATGTCTG GTAATGCCAA CCAAGTCGA 1920
 CATGGGTCTT AGGACACTGA CCACCTCACA TGCCATACCC TCAGTTAAGC ATGTTAACAT 1980
 TTATAGGAGG AAAAAATCA CTTTGGGAGA AAATAAAATT CAACTCAAGC ATAAAGCTTC 2040
 TGTTTACTCA GGCCTTCTAA AAAGCAGGTT AAAATGCTCT AAAATGAGAA AGCCTGTGGT 2100

TTCAC TTATT TATATAACTC ACTGGGACAT TGCCAAATGA GTAAGCACTT AATTCGCTGC 2160
TTCTGAGACT TCTCTGTCAA AACAGCCCCA CTGATAATAT TAGACAGAAC GAGAATGCAG 2220
GGGTCTCTTC CCTCCCCTGG GGTTTAGGAA GCTCATGAGG AGCTCGGCTT AAAATGTCTT 2280
TGATGTCTCT TCCTTTGTCT CAAAAAGTAA TGTCAATTTT ATATACTATT TCAATATTAC 2340
TATCTGCATT TGTTTTAATA TAAAAATGTT TGCTGCCTAC CTTTTTCTCC CAAAAAATCT 2400
TTAAGTAAAG ATGATCTGGG AAAATGAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2460
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2520
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2580
AAAAAAAAAA AAAAAAAGC GGCCGCAGGT CTAGAATTCA ATCGGAAGGT ATATAGCTTA 2640
TTTGTTGCTT TTCATTGTAA TTTAACATGG TTAATGGTTA ATTACTATTT AACACACATT 2700
TCAAATGAAT ATTATTTGGG GGATTAGATT GAGTGAAATT AACCTGCTAT TAAATAGTAA 2760
ACTTTTCCTC TGGAGTCACT TTTTTCCTCC TTCAAAGTAT GTTACTGAGG AAGTAAACTT 2820
TTTTTTTTTT TTTTGGTTTT TGTTTTTTGA GACACAGTCT CGCTCTGTTG CCCAGGCTGC 2880
TGGAGTGCCG TGGCGCAATC TCGGCTCACT GCAACCTCCG CCTCCTGGAT TCAAACAATT 2940
CTCCTGCTTC AGCCTCCTGA GTAGCTGGGA TTACAGGCAC ATGCCACCAC GCCCGGCTAA 3000
TTTTTGTAAT TTTAGTAGAG ACTGGGTTTC ACCATGTTGG TCAGGCTGGT CTCAAACCTC 3060
TGACCTCGTG ATCCACCCGC CTCGGCCTCC CAAATCCTG GGATTACAGG CGCGAGCCAC 3120
CACACCCGGC TGGAAGTAAA CATTTTAAAA GCTACTTTTA CTCATTCTAG CCTTGTAGAA 3180
TGACCATGTC AGCTTGAGGG ACCTAGTTCT TACCTTTTCT TGCAACCAAC ACATTGCAA 3240
TTGTGTCTGG TATGCTTGTT CCTGCTGCTA ATAAAGTAAG GCCCATTACT GTATCGGGAA 3300
TTTCTAGTGT TTCCCTGTGA ATAAACAGAT ATTTCAAAGT ACAAACTTTA AAGATTCACT 3360
AACCATCCTT TGCAGTTATT TTGGATATTT CCTTCGTGAA CAAAAATAAA ATAGGCACAT 3420
TTAGAATTCA GAGCCAATAT GTGCTTGCTT ATTAGTTTTT TAGCTAGCAA CATATTTGAA 3480
TCAGGCTGGT AATTCGGGTA ACCCAGGTAG CACAGATTTT TAATGACATA TYTAAAGATA 3540
CGTAACAGCT AAAATTTCTG CCAGTGAGAA ATTTTCTGTG TTGATATTTT TTACAAAAGA 3600
TGTTTATGTC CACCATTATY TTCATTCAGG GGCTGTGCTG AATATTTGAT AATGAGACTG 3660
ATCATTCGCG TTTTCTTTT TTAATAATAT TAGGCAGAGT TAAGCAAATT AATTATAGCT 3720
ATCTTTAAGC TATAAATGTG TTAACATGTA TATATACCAT TTATTATGTT CTACTTTAGT 3780

GATATACCTT AATTTAGTGG GCTTTGGCAG GCGGGGGGAG GGGGAACGTT CATTAATCTC 3840
 TGAGGAAAAC AAAACCTGTT TTCTACTTGA GTCTAACATA TGGTCCCAAT TTATTAATAC 3900
 TTCTGTTAAA TTTGATGTCA GGTCAACATT TTTCAGAAAT GTATTTATTC TCAGAAACAG 3960
 AACCAGAGAG AAGTTAAACA AAAGGTTATG TAACTGTTCC TTTAATGTTG TAATTGAAAA 4020
 CTTGGTTTATG CGTCTTTTTT TTCTTTCTCT TTTTTTTTCT TAAAATGCCA ACTAAAATAA 4080
 TTAGAAAGTA GCTTATTTAT TGCATGCTTA TACATTGATA TTGGAATTGG AATTGGTTGT 4140
 TAATTTCTGT TACTGGCTTT GCTAGAATTC ATATGTGCAT AAATAACACT AATATTTATC 4200
 ATCTTGGAAG AAAAAAAAAA AAAAAAAAAA AAAAAA 4237

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Tyr | Ile | Tyr | His | Leu | Leu | Cys | Ser | Thr | Leu | Val | Ile | Tyr | Leu | Asn |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Val | Gly | Phe | Gly | Arg | Ala | Gly | Glu | Gly | Glu | Arg | Ser | Leu | Ile | Ser |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Glu | Glu | Asn | Lys | Thr | Cys | Phe | Leu | Leu | Glu | Ser | Asn | Ile | Trp | Ser | Gln |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Phe | Ile | Asn | Thr | Ser | Val | Lys | Phe | Asp | Val | Arg | Ser | Thr | Phe | Phe | Arg |
| | 50 | | | | | 55 | | | | 60 | | | | | |
| Asn | Val | Phe | Ile | Leu | Arg | Asn | Arg | Thr | Arg | Glu | Lys | Leu | Asn | Lys | Arg |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| Leu | Cys | Asn | Cys | Ser | Phe | Asn | Val | Val | Ile | Glu | Asn | Leu | Val | | |
| | | | 85 | | | | | | 90 | | | | | | |

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TNTTGAAGACT GTTGCTTGTT TGGAATGT

29

- (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CNCCATCTAAT GGGATGATGG GTTCTTGA

29

- (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ANTTTCCGTCA CCTCGTTTCGC CTGCTGCT

29

- (2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GNATACGAGGG GTTCCCATGG CTTCTTCT

29

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TNTACGACGAC ATCCAACAAT CACACTGG

29

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TNGTCCGGTTG GAATGAGGTG AGGCAGTG

29

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "olgionucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GNTCCTCACTA TATACTTCTG GAACAACT

29

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GNCCTAAGAGT GTAACACTG GCCTGACC

29

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TNTCCTCGTGC TTCAGGCCAC TGTAATGT

29

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ANGCCCACTAA ATTAAGGTAT ATCACTAA

29

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Trp Gly Leu Gly Thr Thr Ser Ser Phe Arg Trp Tyr Ser Ser Asp

1

10

15

20

25

30

35

40

45

50

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2199 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO33:

| | | | | | | |
|-------------|-------------|-------------|------------|------------|------------|-----|
| AGTTTGGCAGG | TGGAGAGGCCA | GGTTGGGAGG | GAAAGTCGGG | GGAGGACGCG | GAAGAGGAGC | 60 |
| TGTGGGAAGG | GGGAGGAGGG | AGGGAGGAAA | AGAGGAGGAG | GCGGAGGAGA | ACTGAGCAGA | 120 |
| GCAGAGCATC | GAGCCAAAGG | GGAGATGAGT | TTGTCTGTCC | TCTGCTGAGG | CTACGGCCCG | 180 |
| GCCTAGGGAA | CTGGGAGCTT | GGTGGAAGC | GACACCCGTG | GAAGTGGGAG | GAGGTGGCGC | 240 |
| CGGGACTTTA | ACCCCTTG TG | GGCTCTGCGG | CAGGGGATTT | AACCCTTTGT | GGATCTGGCC | 300 |
| CCTCGGAGGC | AGCGTCATCG | G TAGTTTTAA | CCCCTTCGGG | GCTGGGTTTC | ACGCACTGGA | 360 |
| CTTACCCTCA | TCACCTTGCT | CACCAACTCC | TTTATTGGGG | TGCTCCGCTT | GGAGGTTTGA | 420 |
| GGCCACCTC | CGCCATTAC | GTACTGTTCC | TGCCGCTGCA | CCCCCTTGGA | CCCGCTAGCT | 480 |
| GGCCGCACTG | TGGGCGCTTA | ACCCTTTACT | GACTTGAGCT | CCCCAGATTG | CAGTTGGAGT | 540 |
| TTGCTGATAG | AAGGACTAGC | TAAAGGCGTC | ACTGCAGGAA | TTACAAACTG | AAGAGGACTC | 600 |
| TGTTGGACTG | TTTTTTTTTT | CTTTTTCTTT | TTTTTAAGAA | AAACCCATTT | TTTTCCTTAA | 660 |
| GGACTTACTA | GCCAAAATTT | CTTAAACTTC | GAGGACTCTA | CTAGCCATGG | CCGAGCCATT | 720 |
| CTTGTCAGAA | TATCAACACC | AGCCTCAAAC | TAGCAACTGT | ACAGGTGCTG | CTGCTGTCCA | 780 |
| GGAAGAGCTG | AACCCTGAGC | GCCCCCAGG | CGCGGAGGAG | CGGGTGCCCG | AGGAGGACAG | 840 |
| TAGGTGGCAA | TCGAGAGCGT | TCCCCAGTT | GGGTGGCCGT | CCGGGGCCCG | AGGGGGAAGG | 900 |
| GAGCCTGGAA | TCCCAACCAC | CTCCCTTGCA | GACCCAGGCC | TGTCCAGAAT | CTAGCTGCCT | 960 |

| | |
|---|------|
| GAGAGAGGGC GAGAAGGGCC AGAATGGGA CACTCGTCC GCTGGCGGCG ACTTCCCGCC | 1020 |
| GCCGGCAGAA GTGGAACCGA CGCCCGAGGC CGAGCTGCTC GCCCAGCCTT GTCATGACTC | 1080 |
| CGAGGCCAGT AAGTTGGGGG CTCCTGCCGC AGGGGGCGAA GAGGAGTGGG GACAGCAGCA | 1140 |
| GAGACAGCTG GGAAGAAAA AACATAGGAG ACGCCCGTCC AAGAAGAAGC GGCATTGGAA | 1200 |
| ACCGTACTAC AAGCTGACCT GGGAAGAGAA GAAAAAGTTC GACGAGAAAC AGAGCCTTCG | 1260 |
| AGCTTCAAGG ATCCGAGCCG AGATGTTTCG CAAGGGCCAG CCGGTCGCGC CCTATAACAC | 1320 |
| CACGCAGTTC CTCATGGATG ATCACGACCA GGAGGAGCCG GATCTCAAAA CCGGCCTGTA | 1380 |
| CTCCAAGCGG GCCGCCGCCA AATCCGACGA CACCAGCGAT GACGACTTCA TGGAAGAAGG | 1440 |
| GGGTGAGGAG GATGGGGGCA GCGATGGGAT GGGAGGGGAC GGCAGCGAGT TTCTGCAGCG | 1500 |
| GGACTTCTCG GAGACGTACG AGCGGTACCA CACGGAGAGC CTGCAGAACA TGAGCAAGCA | 1560 |
| GGAGCTCATC AAGGAGTACC TGGAAC TGGA GAAGTGCC TC CGCATGG AGGACGAGAA | 1620 |
| CAACCGGCTG CGGCTGGAGA GCAAGCGGCT GGGTGGCGAC GACGCGCGTG TGCGGGAGCT | 1680 |
| GGAGCTGGAG CTGGACCGGC TGCGCGCCGA GAACCTCCAG CTGCTGACCG AGAACGAACT | 1740 |
| GCACCGGCAG CAGGAGCGAG CGCCGCTTTC CAAGTTTGGA GACTAGACTG AAACTTTTTT | 1800 |
| GGGGGAGGGG GCAAAGGGGA CTTTTTACAG TGATGGAATG TAACATTATA TACATGTGTA | 1860 |
| TATAAGACAG TGGACCTTTT TATGACACAT AATCAGAAGA GAAATCCCCC TGGCTTTGGT | 1920 |
| TGGTTTCGTA AATTTAGCTA TATGTAGCTT GCGTGCTTTC TCCTGTTCTT TTAATTATGT | 1980 |
| GAAACTGAAG AGTTGCTTTT CTGTGTTTCC TTTT TAGAAG TTTT TTTTCT TAATGTGAAA | 2040 |
| GTAATTTGAC CAAGTTATAA TGCATTTTTG TTTT TAACAA ATCCCTCCT TAAACGGAGC | 2100 |
| TATAAGGTGG CCAAATCTGA GAACAATTAA ATTCATTTTA GTTATAATAA ATTTAATATT | 2160 |
| TGTAAATGTA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA | 2199 |

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ala Glu Pro Phe Leu Ser Glu Tyr Gln His Gln Pro Gln Thr Ser

| | | | |
|---|-----|-----|-----|
| 1 | 5 | 10 | 15 |
| Asn Cys Thr Gly Ala Ala Ala Val Gln Glu Glu Leu Asn Pro Glu Arg | 20 | 25 | 30 |
| Pro Pro Gly Ala Glu Glu Arg Val Pro Glu Glu Asp Ser Arg Trp Gln | 35 | 40 | 45 |
| Ser Arg Ala Phe Pro Gln Leu Gly Gly Arg Pro Gly Pro Glu Gly Glu | 50 | 55 | 60 |
| Gly Ser Leu Glu Ser Gln Pro Pro Pro Leu Gln Thr Gln Ala Cys Pro | 65 | 70 | 75 |
| Glu Ser Ser Cys Leu Arg Glu Gly Glu Lys Gly Gln Asn Gly Asp Asp | 85 | 90 | 95 |
| Ser Ser Ala Gly Gly Asp Phe Pro Pro Pro Ala Glu Val Glu Pro Thr | 100 | 105 | 110 |
| Pro Glu Ala Glu Leu Leu Ala Gln Pro Cys His Asp Ser Glu Ala Ser | 115 | 120 | 125 |
| Lys Leu Gly Ala Pro Ala Ala Gly Gly Glu Glu Glu Trp Gly Gln Gln | 130 | 135 | 140 |
| Gln Arg Gln Leu Gly Lys Lys Lys His Arg Arg Arg Pro Ser Lys Lys | 145 | 150 | 155 |
| Lys Arg His Trp Lys Pro Tyr Tyr Lys Leu Thr Trp Glu Glu Lys Lys | 165 | 170 | 175 |
| Lys Phe Asp Glu Lys Gln Ser Leu Arg Ala Ser Arg Ile Arg Ala Glu | 180 | 185 | 190 |
| Met Phe Ala Lys Gly Gln Pro Val Ala Pro Tyr Asn Thr Thr Gln Phe | 195 | 200 | 205 |
| Leu Met Asp Asp His Asp Gln Glu Glu Pro Asp Leu Lys Thr Gly Leu | 210 | 215 | 220 |
| Tyr Ser Lys Arg Ala Ala Ala Lys Ser Asp Asp Thr Ser Asp Asp Asp | 225 | 230 | 235 |
| Phe Met Glu Glu Gly Gly Glu Glu Asp Gly Gly Ser Asp Gly Met Gly | 245 | 250 | 255 |
| Gly Asp Gly Ser Glu Phe Leu Gln Arg Asp Phe Ser Glu Thr Tyr Glu | 260 | 265 | 270 |
| Arg Tyr His Thr Glu Ser Leu Gln Asn Met Ser Lys Gln Glu Leu Ile | 275 | 280 | 285 |
| Lys Glu Tyr Leu Glu Leu Glu Lys Cys Leu Ser Arg Met Glu Asp Glu | 290 | 295 | 300 |
| Asn Asn Arg Leu Arg Leu Glu Ser Lys Arg Leu Gly Gly Asp Asp Ala | 305 | 310 | 315 |
| | | | 320 |

Arg Val Arg Glu Leu Glu Leu Glu Leu Asp Arg Leu Arg Ala Glu Asn
325 330 335

Leu Gln Leu Leu Thr Glu Asn Glu Leu His Arg Gln Gln Glu Arg Ala
340 345 350

Pro Leu Ser Lys Phe Gly Asp
355

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGCTAGGCCG CGAGCTTAGT CCTGGGAGCC GCCTCCGTCG CCGCCGTCAG AGCCGCCCTA 60
TCAGATTATC TTAACAAGAA AACCAACTGG AAAAAAAAAAT GAAATTCCTT ATCTTCGCAT 120
TTTTCGGTGG TGTTACCTT TTATCCCTGT GCTCTGGGAA AGCTATATGC AAGAATGGCA 180
TCTCTAAGAG GACTTTTGAA GAAATAAAAG AAGAAATAGC CAGCTGTGGA GATGTTGCTA 240
AAGCAATCAT CAACCTAGCT GTTTATGGTA AAGCCCAGAA CAGATCCTAT GAGCGATTGG 300
CACTTCTGGT TGATACTGTT GGACCCAGAC TGAGTGGCTC CAAGAACCTA GAAAAAGCCA 360
TCCAAATTAT GTACCAAAAC CTGCAGCAAG ATGGGCTGGA GAAAGTTCAC CTGGAGCCAG 420
TGAGAATACC CCACTGGGAG AGGGGAGAAG AATCAGCTGT GATGCTGGAG CCAAGAATTC 480
ATAAGATAGC CATCCTGGGT CTTGGCAGCA GCATTGGGAC TCCTCCAGAA GGCATTACAG 540
CAGAAGTTCT GGTGGTGACC TCTTTCGATG AACTGCAGAG AAGGGCCTCA GAAGCAAGAG 600
GGAAGATTGT TGTTTATAAC CAACCTTACA TCAACTACTC AAGGACGGTG CAATACCGAA 660
CGCAGGGGGC GGTGGAAGCT GCCAAGGTGG GGGCTTTGGC ATCTCTCATT CGATCCGTGG 720
CCTCCTTCTC CATCTACAGT CCTCACACAG GTATTCAGGA ATACCAGGAT GGCGTGCCCA 780
AAATTCCAAC AGCCTGTATT ACGGTGGAAG ATGCAGAAAT GATGTCAAGA ATGGCTTCTC 840
ATGGGATCAA AATTGTCATT CAGCTAAAGA TGGGGGCAAA GACCTACCCA GATACTGATT 900
CCTTCAACAC TGTAGCAGAG ATCACTGGGA GCAAATATCC AGAACAGGTT GTACTGGTCA 960
GTGGACATCT GGACAGCTGG GATGTTGGGC AGGGTGCCAT GGATGATGGC GGTGGAGCCT 1020
TTATATCATG GGAAGCACTC TCACTTATTA AAGATCTTGG GCTGCGTCCA AAGAGGACTC 1080

TGCGGCTGGT GCTCTGGACT GCAGAAGAAC AAGGTGGAGT TGGTGCCTTC CAGTATTATC 1140
 AGTTACACAA GGTAATATT TCCAACCTACA GTCTGGTGAT GGAGTCTGAC GCAGGAACCT 1200
 TCTTACCCAC TGGGCTGCAA TTTACTGGCA GTGAAAAGGC CAGGGCCATC ATGGAGGAGG 1260
 TTATGAGCCT GCTGCAGCCC CTCAATATCA CTCAGGTCCT GAGCCATGGA GAAGGGACAG 1320
 ACATCAACTT TTGGATCCAA GCTGGAGTGC CTGGAGCCAG TCTACTTGAT GACTTATACA 1380
 AGTATTTCTT CTTCCATCAC TCCCACGGAG ACACCATGAC TGTCATGGAT CCAAAGCAGA 1440
 TGAATGTTGC TGCTGCTGTT TGGGCTGTTG TTTCTTATGT TGTTCAGAC ATGGAAGAAA 1500
 TGCTGCCTAG GTCCTAGAAA CAGTAAGAAA GAAACGTTTT CATGCTTCTG GCCAGGAATC 1560
 CTGGGTCTGC AACTTTGGAA AACTCCTCTT CACATAACAA TTTCATCCAA TTCATCTTCA 1620
 AAGCACAACCT CTATTTTCATG CTTTCTGTGA TTATCTTTCT TGATACTTTC CAAATTCTCT 1680
 GATTCTAGAA AAAGGAATCA TTCTCCCCTC CCTCCCACCA CATAGAATCA ACATATGGTA 1740
 GGGATTACAG TGGGGGCATT TCTTTATATC ACCTCTTAAA AACATTGTTT CCACTTTAAA 1800
 AGTAAACACT TAATAAATTT TTGGAAGATC TCTGAAAAAA AAAAAAAAAA A 1851

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Lys Phe Leu Ile Phe Ala Phe Phe Gly Gly Val His Leu Leu Ser
 1 5 10 15
 Leu Cys Ser Gly Lys Ala Ile Cys Lys Asn Gly Ile Ser Lys Arg Thr
 20 25 30
 Phe Glu Glu Ile Lys Glu Glu Ile Ala Ser Cys Gly Asp Val Ala Lys
 35 40 45
 Ala Ile Ile Asn Leu Ala Val Tyr Gly Lys Ala Gln Asn Arg Ser Tyr
 50 55 60
 Glu Arg Leu Ala Leu Leu Val Asp Thr Val Gly Pro Arg Leu Ser Gly
 65 70 75 80
 Ser Lys Asn Leu Glu Lys Ala Ile Gln Ile Met Tyr Gln Asn Leu Gln
 85 90 95

Gln Asp Gly Leu Glu Lys Val His Leu Glu Pro Val Arg Ile Pro His
 100 105 110
 Trp Glu Arg Gly Glu Glu Ser Ala Val Met Leu Glu Pro Arg Ile His
 115 120 125
 Lys Ile Ala Ile Leu Gly Leu Gly Ser Ser Ile Gly Thr Pro Pro Glu
 130 135 140
 Gly Ile Thr Ala Glu Val Leu Val Val Thr Ser Phe Asp Glu Leu Gln
 145 150 155 160
 Arg Arg Ala Ser Glu Ala Arg Gly Lys Ile Val Val Tyr Asn Gln Pro
 165 170 175
 Tyr Ile Asn Tyr Ser Arg Thr Val Gln Tyr Arg Thr Gln Gly Ala Val
 180 185 190
 Glu Ala Ala Lys Val Gly Ala Leu Ala Ser Leu Ile Arg Ser Val Ala
 195 200 205
 Ser Phe Ser Ile Tyr Ser Pro His Thr Gly Ile Gln Glu Tyr Gln Asp
 210 215 220
 Gly Val Pro Lys Ile Pro Thr Ala Cys Ile Thr Val Glu Asp Ala Glu
 225 230 235 240
 Met Met Ser Arg Met Ala Ser His Gly Ile Lys Ile Val Ile Gln Leu
 245 250 255
 Lys Met Gly Ala Lys Thr Tyr Pro Asp Thr Asp Ser Phe Asn Thr Val
 260 265 270
 Ala Glu Ile Thr Gly Ser Lys Tyr Pro Glu Gln Val Val Leu Val Ser
 275 280 285
 Gly His Leu Asp Ser Trp Asp Val Gly Gln Gly Ala Met Asp Asp Gly
 290 295 300
 Gly Gly Ala Phe Ile Ser Trp Glu Ala Leu Ser Leu Ile Lys Asp Leu
 305 310 315 320
 Gly Leu Arg Pro Lys Arg Thr Leu Arg Leu Val Leu Trp Thr Ala Glu
 325 330 335
 Glu Gln Gly Gly Val Gly Ala Phe Gln Tyr Tyr Gln Leu His Lys Val
 340 345 350
 Asn Ile Ser Asn Tyr Ser Leu Val Met Glu Ser Asp Ala Gly Thr Phe
 355 360 365
 Leu Pro Thr Gly Leu Gln Phe Thr Gly Ser Glu Lys Ala Arg Ala Ile
 370 375 380
 Met Glu Glu Val Met Ser Leu Leu Gln Pro Leu Asn Ile Thr Gln Val
 385 390 395 400
 Leu Ser His Gly Glu Gly Thr Asp Ile Asn Phe Trp Ile Gln Ala Gly

| | | | |
|---|-----|-----|-----|
| | 405 | 410 | 415 |
| Val Pro Gly Ala Ser Leu Leu Asp Asp Leu Tyr Lys Tyr Phe Phe Phe | | | |
| | 420 | 425 | 430 |
| His His Ser His Gly Asp Thr Met Thr Val Met Asp Pro Lys Gln Met | | | |
| | 435 | 440 | 445 |
| Asn Val Ala Ala Ala Val Trp Ala Val Val Ser Tyr Val Val Ala Asp | | | |
| | 450 | 455 | 460 |
| Met Glu Glu Met Leu Pro Arg Ser | | | |
| | 465 | 470 | |

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1076 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

| | |
|---|-----|
| CAGAAGTTCA AGGGCCCCCG GCCTCCTGCG CTCCTGCCGC CGGGACCCTC GACCTCCTCA | 60 |
| GAGCAGCCGG CTGCCGCCCC GGGAAGATGG CGAGGAGGAG CCGCCACCGC CTCCTCCTGC | 120 |
| TGCTGCTGCG CTACCTGGTG GTCGCCCTGG GCTATCATAA GGCCTATGGG TTTTCTGCCC | 180 |
| CAAAAGACCA ACAAGTAGTC ACAGCAGTAG AGTACCAAGA GGCTATTTTA GCCTGCAAAA | 240 |
| CCCCAAAGAA GACTGTTTCC TCCAGATTAG AGTGGAAGAA ACTGGGTCGG AGTGTCTCCT | 300 |
| TTGTCTACTA TCAACAGACT CTTCAGGTG ATTTTAAAAA TCGAGCTGAG ATGATAGATT | 360 |
| TCAATATCCG GATCAAAAAT GTGACAAGAA GTGATGCGGG GAAATATCGT TGTGAAGTTA | 420 |
| GTGCCCCATC TGAGCAAGGC CAAAACCTGG AAGAGGATAC AGTCACTCTG GAAGTATTAG | 480 |
| TGGCTCCAGC AGTTCCATCA TGTGAAGTAC CCTCTTCTGC TCTGAGTGGA ACTGTGGTAG | 540 |
| AGCTACGATG TCAAGACAAA GAAGGGAATC CAGCTCCTGA ATACACATGG TTTAAGGATG | 600 |
| GCATCCGTTT GCTAGAAAAT CCCAGACTTG GCTCCCAAAG CACCAACAGC TCATACACAA | 660 |
| TGAATACAAA AACTGGAACT CTGCAATTTA ATACTGTTTC CAACTGGAC ACTGGAGAAT | 720 |
| ATTCTGTGA AGCCCGCAAT TCTGTTGGAT ATCGCAGGTG TCCTGGGAAA CGAATGCAAG | 780 |
| TAGATGATCT CAACATAAGT GGCATCATAG CAGCCGTAGT AGTTGTGGCC TTAGTGATTT | 840 |
| CCGTTTGTGG CCTTGGTGTA TGCTATGCTC AGAGGAAAGG CTACTTTTCA AAAGAAACCT | 900 |

CCTTCCAGAA GAGTAATTCT TCATCTAAAG CCACGACAAT GAGTGAAAAT GATTTCAAGC 960
 ACACAAAATC CTTTATAATT TAAAGACTCC ACTTTAGAGA TACACCAAAG CCACCGTTGT 1020
 TACACAAGTT ATTAAACTAT TATAAACTC AAAAAAAAAA AAAAAAAAAA AAAAAA 1076

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 298 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Arg | Arg | Ser | Arg | His | Arg | Leu | Leu | Leu | Leu | Leu | Arg | Tyr | 1 | 5 | 10 | 15 |
| Leu | Val | Val | Ala | Leu | Gly | Tyr | His | Lys | Ala | Tyr | Gly | Phe | Ser | Ala | Pro | 20 | 25 | 30 |
| Lys | Asp | Gln | Gln | Val | Val | Thr | Ala | Val | Glu | Tyr | Gln | Glu | Ala | Ile | Leu | 35 | 40 | 45 |
| Ala | Cys | Lys | Thr | Pro | Lys | Lys | Thr | Val | Ser | Ser | Arg | Leu | Glu | Trp | Lys | 50 | 55 | 60 |
| Lys | Leu | Gly | Arg | Ser | Val | Ser | Phe | Val | Tyr | Tyr | Gln | Gln | Thr | Leu | Gln | 65 | 70 | 75 |
| Gly | Asp | Phe | Lys | Asn | Arg | Ala | Glu | Met | Ile | Asp | Phe | Asn | Ile | Arg | Ile | 85 | 90 | 95 |
| Lys | Asn | Val | Thr | Arg | Ser | Asp | Ala | Gly | Lys | Tyr | Arg | Cys | Glu | Val | Ser | 100 | 105 | 110 |
| Ala | Pro | Ser | Glu | Gln | Gly | Gln | Asn | Leu | Glu | Glu | Asp | Thr | Val | Thr | Leu | 115 | 120 | 125 |
| Glu | Val | Leu | Val | Ala | Pro | Ala | Val | Pro | Ser | Cys | Glu | Val | Pro | Ser | Ser | 130 | 135 | 140 |
| Ala | Leu | Ser | Gly | Thr | Val | Val | Glu | Leu | Arg | Cys | Gln | Asp | Lys | Glu | Gly | 145 | 150 | 155 |
| Asn | Pro | Ala | Pro | Glu | Tyr | Thr | Trp | Phe | Lys | Asp | Gly | Ile | Arg | Leu | Leu | 165 | 170 | 175 |
| Glu | Asn | Pro | Arg | Leu | Gly | Ser | Gln | Ser | Thr | Asn | Ser | Ser | Tyr | Thr | Met | 180 | 185 | 190 |
| Asn | Thr | Lys | Thr | Gly | Thr | Leu | Gln | Phe | Asn | Thr | Val | Ser | Lys | Leu | Asp | | | |

| | | |
|---|-------------------------------------|-----|
| 195 | 200 | 205 |
| Thr Gly Glu Tyr Ser Cys Glu | Ala Arg Asn Ser Val Gly Tyr Arg Arg | |
| 210 | 215 | 220 |
| Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile | | |
| 225 | 230 | 235 |
| Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu | | |
| 245 | 250 | 255 |
| Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser | | |
| 260 | 265 | 270 |
| Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn | | |
| 275 | 280 | 285 |
| Asp Phe Lys His Thr Lys Ser Phe Ile Ile | | |
| 290 | 295 | |

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2522 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

| | |
|--|-----|
| GAAAGGTTGT GTAGCTTGCC CTGGTTGCAT AGTTAAACGA GGGCTAGAAA CAGGACTAGG | 60 |
| AGTCAGGCCT GTCCAGCTGG AAAACTTGGG TTTTCTAGAA GGGGTACCCT GGCCTCCTGC | 120 |
| GGAGCCTGCT GTGGGACTCT GCAGAACACA ATTCAAGGCC AGACTGAACA CTAGCCTGAA | 180 |
| CCTGCCCTGA GAATCCCTCT AAGCCGACCT ACTCCACAGC TGTCTGACT GTGTAAGCGA | 240 |
| GATGATGATT AGTGATCAGA CGAAAGGATT CCTGTCATTG GTAACCCTCT CAAAGTATTT | 300 |
| GGAAAACAGT TCAATTTTCA TCTATTTTCAG AAGCACGCCG TGGTGTCTAT TGAGGCTCAC | 360 |
| CTGCATTGAA TTCCTTCCTT TTTATGTTGC GATCTCCCAA GATTGCATTG TGGAGTGTTT | 420 |
| TCGAATCCAT TTTGAAATCC CCGTGCGTGC GCTATGCAGG CCTCAGTCTT TTTCCATTCC | 480 |
| ATTCTTAACT CTACTTTTCA CGGAAGCAGT GTTTTACCCC GACACTGGCT TGCCTAGGAC | 540 |
| CTTGTGCTCT GCACAACTAG CAGGGCCCGG CAGGATGTAC TGAATTCTTG CTCTCGTGTC | 600 |
| CAGCTGGACG GTGATGGCTT TCAAGTCCTT GGCTGTTGGG AGCTTACTAT AAATGTTCGT | 660 |
| CTTGGCTACA AACTCTCCAC TCTTTCCTCG GCACTCTCTC AGCATTGCCA CCACTGTCTT | 720 |

TCCTCTTGGC CAACTGTTTT CTTTACTTAG GCTTTCCTT GCTAGAAAGT CCAGGTAAC 780

TTCTCCACGG GACCTGGTTT CTTTCGCACA TCCCAGCTGG CCTCGAGGAA AGGTAGCTCT 840

TCCAAATCAG AGAATCTGGA TGCTGGGCTG GGCTCTGCAC CAACCAGCTG GGCCGCTTCA 900

CCCGCTGGGC CCCAAACTAC TCATCTGTGA AGCGAAGGCA CCGCGCTTGA TGCCTTCTGC 960

AACGTTCTTC AGTTTGAAAA TCCTTCTGTT TCGTTGGGGA TATTTACGG CCTCTTCTCA 1020

AGGTTGCACT TTTGCCAGCT GCCAGGGATC GTCTCAAAAC AGGTTCTTAG TGCATTCATA 1080

GCTTGAGCTG CTGTCTTGAA AGTAGTACAT TCCTTTTTCT GCCAACTTTT TTCTGAGAAA 1140

GTTTTTGAAT GCACACGTGC ACCCAACAGA GTGAGAGTGG CTGTTAAGAG AGAGGGCGCC 1200

ATTTCTTTTG CCCTCCAGCC TGTCCCTGTG CACCCTGGAG GGGCCCGTTT TTTCCACCGC 1260

TTAGATAAAA TCTAGGGCAA GTTCCTGAAC TTCTCTTGTC TCTCTCAGGT AACAAAAATT 1320

CTTTTGGGCT CCTTTAGTCA CAAAGATATT CACGATTTCA GGTATTAAAG TGCCAGCCCC 1380

TGGGTGATTG TCAAAATTCT GAACTTGATT TAAAGTGGCA CCTCCTCTCA CAGTCTTCGG 1440

GAGGGAGAGA CCGGAGCCAG GAGTGCAGCG TGTGTGCTGG GGTCTGTCGT GGCCCACTCC 1500

ACACCTGCTG GGTGGATCCG GCTGGTGCCC CATGGGCGCC TCTGAGATGC CCCTCCCCAC 1560

CCCATCAGTG GCGCTGTCTC ACCTGCAGGC TGTCTCACA GGTGGTCCCC CCTCACTCCT 1620

CCTGCAGCCC CAGTTCCTGG CTGTTTATTG TTATTGGGAC CCGTCACCCT CCTGGAGGCG 1680

GTCCCAGCCG AGCCCCCTTA AGACAGCACC AGGCTGGCTC CACTTGGCCC CCGCTGGTTC 1740

AGGGAAGTGC TGCTGCAGCC GTTTAGTTTG ACAAAGGAGG CAGCGAGGCC GTCTCATTGG 1800

TAGCCCTCTC CTGGCTTGCC CAGCCACCAC CTCACCTCGA TTCCTCCCAG GCCTGGGTCC 1860

AGCACCAGCC TAGGAAGAGG GTGCCCCATG CTGTCTAGCT CTTCTTCGGG ATGGGGGGCT 1920

CCAGGTTTCCT TGGTATTTTG CTTTGGCCTT TGGAGCCTCA GTCAAACTG AGGAAAGGTG 1980

TCATTTTCAC ATCTCGTCAC ACGTACAGTG ACTGCAACTA AAAGCACAGG CTTTGTAGAA 2040

ACAGACATGG GTTCAGGCCC CAGCTCCACC ATTCACAAGG TGTGTGGCTT CCTGCAAGGT 2100

ACCTTCATCT CTGAGTTACC TGACTCCATC TGAGTTTCCT TCTTGTAATA CTGGCATCCA 2160

TGAAAGTGGC TACCTCGAAG GGCGTGAAGA TGAAATGAGG TGGAAAGTAG GTAGCCCCCG 2220

AATGAGGGAA GCATTGAGTG AGAGCTGGCC CTCTGACCCT TCTAAAAGAA CACAGCCAAC 2280

TTTTTAACT GTCTTTCCAG AAAGAGATGG AAAACTTCGA AGCCCTTTT CACTGCCTTG 2340

CCAAGCAGTT CCACCAGCTG TACCGGGAGA AGGTGGAGGT TTTCCGGGCC CTGGCATGAC 2400

GAGCTGGAGC AGATCGTGCT GCACAACCGG AGAAGACAGA ATTACCTCTG CTCTTTTAAT 2460

ATATAATGAT GGCTTTAAAT AAAATTAGGA GAAAATGTCA AAAAAAAAAA AAAAAAAAAA 2520
AA 2522

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Met Ile Ser Asp Gln Thr Lys Gly Phe Leu Ser Leu Val Thr Leu
1 5 10 15
Ser Lys Tyr Leu Glu Asn Ser Ser Ile Phe Ile Tyr Phe Arg Ser Thr
20 25 30
Pro Trp Cys Leu Leu Arg Leu Thr Cys Ile Glu Phe Leu Pro Phe Tyr
35 40 45
Val Ala Ile Ser Gln Asp Cys Ile Val Glu Cys Phe Arg Ile His Phe
50 55 60
Glu Ile Pro Val Arg Ala Leu Cys Arg Pro Gln Ser Phe Ser Ile Pro
65 70 75 80
Phe Leu Thr Leu Leu Ser Thr Glu Ala Val Phe Tyr Pro Asp Thr Gly
85 90 95
Leu Pro Arg Thr Leu Cys Ser Ala Gln Leu Ala Gly Pro Gly Arg Met
100 105 110
Tyr

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1962 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCCGGGCCCC AGCCTTCTCC AGAACCCCTG CTACCCACGA CTAAGCCCCG AACAATCTGC 60
CCTTGGGCTT GTTCTCTTCG CAGTTGTCGG CCCTGGGCGG GGAGCTGGAG TCCCAGACTC 120

| | | | | | | |
|------------|-------------|------------|-------------|------------|-------------|------|
| ATAGGTCCCG | GCCCAGCCCC | CGAAGAGCCG | CCTCAGCCGG | GGGGAGTTGC | TCGGACTCAA | 180 |
| ACGTCCAGTC | CTCGTGCGAC | CGCGCTGGGT | CGGAAGTGAG | CAGGCTGAGG | CCACCATGGA | 240 |
| GCAGTGTGCG | TGCGTGGAGA | GAGAGCTGGA | CAAGGTCCTG | CAGAAGTTCC | TGACCTACGG | 300 |
| GCAGCACTGT | GAGCGGAGCC | TGGAGGAGCT | GCTGCACTAC | GTGGGCCAGC | TGCGGGCTGA | 360 |
| GCTGGCCAGC | GCAGCCCTCC | ARGGGACCCC | TCTCTCAGCC | ACCTCTCTCT | TGGTGATGTC | 420 |
| ACAGTGCTGC | CGGAAGATCA | AAGATACGGT | GCAGAACTG | GCTTCGGAMC | ATAAGGACAT | 480 |
| TCACAGCAGT | GTATCCCGAG | TGGGCAAAGC | CATTGACAGG | AACTTCGACT | CTGAGATCTG | 540 |
| TGGTGTTGTG | TCAGATGCGG | TGTGGGACGC | GCGGGAACAG | CAGCAGCAGA | TCCTGCAGAT | 600 |
| GGCCATCGTG | GAACACCTGT | ATCAGCAGGG | CATGCTCAGC | GTGGCCGAGG | AGCTGTGCCA | 660 |
| GGAATCAACG | CTGAATGTGG | ACTTGATTTT | CAAGCAGCCT | TTCCTAGAGT | TGAATCGAAT | 720 |
| CCTGGAAGCC | CTGCACGAAC | AAGACCTGGG | TCCTGCGTTG | GAATGGGCCG | TCTCCACAG | 780 |
| GCAGCGCCTG | CTGGAActCA | ACAGCTCCCT | GGAGTTCAAG | CTGCACCGAC | TGCAC TTCAT | 840 |
| CCGCCTCTTG | GCAGGAGGCC | CCGCGAAGCA | GCTGGAGGCC | CTCAGCTATG | CTCGGCACTT | 900 |
| CCAGCCCTTT | GCTCGGCTGC | ACCAGCGGGA | GATCCAGGTG | ATGATGGGCA | GCCTGGTGTA | 960 |
| CCTGCGGCTG | GGCTTGAGAG | AGTCACCCTA | CTGCCACCTG | CTGGACAGCA | GCCACTGGGC | 1020 |
| AGAGATCTGT | GAGACCTTTA | CCCGGGACGC | CTGTTCCCTG | CTGGGGCTTT | CTGTGGAGTC | 1080 |
| CCCCCTTAGC | GTCAGCTTTG | CCTYTGGCTG | TGTGGCGCTG | CCTGTGTTGA | TGAACATCAA | 1140 |
| GGCTGTGATT | GAGCAGCGGC | AGTGCACTGG | GGTCTGGAAT | CACAAGGACG | AGTTACCGAT | 1200 |
| GAGATTGAAC | TAGGCATGAA | GTGCTGGTAC | CACTCCGTGT | TCGCTTGCCC | CATCCTCCGC | 1260 |
| CAGCAGACGT | CAGATTCCAA | CCCTCCCATC | AAGCTCATCT | GTGGCCATGT | TATCTCCCGA | 1320 |
| GATGCACTCA | ATAAGCTCAT | TAATGGAGGA | AAGCTGAAGT | GTCCCTACTG | TCCCATGGAG | 1380 |
| CAGAACCCCG | CAGATGGGAA | ACGCATCATA | TTCTGATTCC | TACCTGGAAG | GAATTTTGTT | 1440 |
| GAAAGGGGTT | TTCACCTGTG | AGCCTTGGTC | TGTCTCGGTA | GGGTGGTCAA | CTTCAGTGGA | 1500 |
| CTGTGGTTGG | TTTCAGAGCG | CCTGGCTGAG | GAGTTCCACT | GAGGGGAGCA | CTGGAGCAGC | 1560 |
| CCTTTGGCAG | AGGCTGAGGA | GGGAGATGGA | CCAGCCCACG | CCTGGCACCT | GGCTCCATGG | 1620 |
| CATAAGGAAA | GGGAGATGCT | GGCCTCTGTG | CTCCTGCTGT | CTTTTCCTGT | TTCTGTTTGC | 1680 |
| GTTTGACTTA | G TAGCAACCG | ACAGAGTGGC | AAGGGATT TG | GTCTTCAGCA | G TAGACATCC | 1740 |
| TTCCACCCCT | GCCCTCAGCC | AAGTCTCTTG | CTGCCATGCC | AATGCTATGT | CCACCCTTGC | 1800 |

CCCTCGGCCC AAGAGTGTCC AGCGGTGGCC CACYTYTTCC TCCCACTACA GCCTCAACAG 1860
TATGTACCAT CTCCCACTGT AAATAGTCCC AGTTAGAACG GAATGCCGTT GTTTTATAAC 1920
TTTGAACAAA TGTATTTACT GCCAAAAAAA AAAAAAAAAA AA 1962

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Glu Gln Cys Ala Cys Val Glu Arg Glu Leu Asp Lys Val Leu Gln
1 5 10 15
Lys Phe Leu Thr Tyr Gly Gln His Cys Glu Arg Ser Leu Glu Glu Leu
20 25 30
Leu His Tyr Val Gly Gln Leu Arg Ala Glu Leu Ala Ser Ala Ala Leu
35 40 45
Gln Gly Thr Pro Leu Ser Ala Thr Leu Ser Leu Val Met Ser Gln Cys
50 55 60
Cys Arg Lys Ile Lys Asp Thr Val Gln Lys Leu Ala Ser Xaa His Lys
65 70 75 80
Asp Ile His Ser Ser Val Ser Arg Val Gly Lys Ala Ile Asp Arg Asn
85 90 95
Phe Asp Ser Glu Ile Cys Gly Val Val Ser Asp Ala Val Trp Asp Ala
100 105 110
Arg Glu Gln Gln Gln Gln Ile Leu Gln Met Ala Ile Val Glu His Leu
115 120 125
Tyr Gln Gln Gly Met Leu Ser Val Ala Glu Glu Leu Cys Gln Glu Ser
130 135 140
Thr Leu Asn Val Asp Leu Asp Phe Lys Gln Pro Phe Leu Glu Leu Asn
145 150 155 160
Arg Ile Leu Glu Ala Leu His Glu Gln Asp Leu Gly Pro Ala Leu Glu
165 170 175
Trp Ala Val Ser His Arg Gln Arg Leu Leu Glu Leu Asn Ser Ser Leu
180 185 190
Glu Phe Lys Leu His Arg Leu His Phe Ile Arg Leu Leu Ala Gly Gly
195 200 205

Pro Ala Lys Gln Leu Glu Ala Leu Ser Tyr Ala Arg His Phe Gln Pro
 210 215 220

Phe Ala Arg Leu His Gln Arg Glu Ile Gln Val Met Met Gly Ser Leu
 225 230 235 240

Val Tyr Leu Arg Leu Gly Leu Glu Lys Ser Pro Tyr Cys His Leu Leu
 245 250 255

Asp Ser Ser His Trp Ala Glu Ile Cys Glu Thr Phe Thr Arg Asp Ala
 260 265 270

Cys Ser Leu Leu Gly Leu Ser Val Glu Ser Pro Leu Ser Val Ser Phe
 275 280 285

Ala Xaa Gly Cys Val Ala Leu Pro Val Leu Met Asn Ile Lys Ala Val
 290 295 300

Ile Glu Gln Arg Gln Cys Thr Gly Val Trp Asn His Lys Asp Glu Leu
 305 310 315 320

Pro Met Arg Leu Asn
 325

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 745 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AAAAACACAA AACCCCGTAA AATCACAAAG AAAATCCAAC ACCAAAGGCG CAGAAGCCGG 60

CTGGCCGTGG TGGGGGCAGC GTAGGCGTAG CATCCCTCTC CTCTCACTTA GCCTGTTGAC 120

TCTTGTTATT ATCATGATAT TCACAAAACG CCGCATGTTT AAAAAGTCAT AGATGTCATC 180

TTCTCTCTGC CCCAGGGAG GAAAGCCACC TTCTCTTGCC CCTTGGCCCC TTTGTCAGGG 240

GCCAGGGGTC TGCCGGGTGG GGGTGCCAAC AGGCCTGGCC CTTTCTCTCC CTGCATCCAG 300

CCATGGGGGC CTCTGCGATT GCCGGAAGGT TGCATGGCTG GTCCCAGGGC CAGCACAGGC 360

CCGAGGCCGG GCTGCCTGGT TTTATTTTTA TTAACTTTA TTTTCTGTTT TATGAGTGTG 420

TGTCCGCCCA CCCCCACCCC CTCAGTGTT AAGTGGGGAG CCCTGGGGGA GTCTCTCCTG 480

CCTCCCAGCC TCTCCAAGA CCTCCCCCT CGTCACCAGC CATCCCTCTG GACCAGGCAG 540

AGGGCGGACC GGGTGGGCAG GGGCCTGAGG GTGGCTCGGG CCAGCCCACC AGCCAATGGA 600
 CCCCTCCTCA GGCCGCCAGT GTCGCCCTGC CCCTTTTAA AACAAAATGC CCTCGTTTGT 660
 AAACCCTTAG ACGCTTGAGA ATAAACCCCT TCCTTTTCTT CCAAAAAAAAA AAAAAAAAAA 720
 AAAAAAAAAA AAAAAAAAAA AAAAA 745

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Gly | Pro | Arg | Ala | Ser | Thr | Gly | Pro | Arg | Pro | Gly | Cys | Leu | Val | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Leu | Phe | Leu | Phe | Asn | Phe | Ile | Phe | Cys | Phe | Met | Ser | Val | Cys | Pro | Pro | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Thr | Pro | Thr | Pro | Phe | Ser | Val | Lys | Trp | Gly | Ala | Leu | Gly | Glu | Ser | Leu | |
| | | | 35 | | | | 40 | | | | | 45 | | | | |
| Leu | Pro | Pro | Ser | Leu | Ser | Gln | Asp | Leu | Pro | Pro | Arg | His | Gln | Pro | Ser | |
| | | | 50 | | | 55 | | | | | 60 | | | | | |
| Leu | Trp | Thr | Arg | Gln | Arg | Ala | Asp | Arg | Val | Gly | Arg | Gly | Leu | Arg | Val | |
| 65 | | | | 70 | | | | | 75 | | | | 80 | | | |
| Ala | Arg | Ala | Ser | Pro | Pro | Ala | Asn | Gly | Pro | Leu | Leu | Arg | Pro | Pro | Val | |
| | | | 85 | | | | | 90 | | | | | 95 | | | |
| Ser | Pro | Cys | Pro | Phe | Leu | Lys | Gln | Asn | Ala | Leu | Val | Cys | Lys | Pro | Leu | |
| | | | 100 | | | | 105 | | | | | 110 | | | | |
| Asp | Ala | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1983 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

| | | | | | | |
|-------------|-------------|-------------|------------|------------|-------------|------|
| TGGCAATAGT | GGTTAGGGAA | GGCTCCTTTG | AGGAAGTGAA | TTTTTAGCTG | AGACTTAAAG | 60 |
| AACAAATGAG | ATTTAGCTAG | AAAAATTGGA | CATGCGATGC | CAAGATGGCA | TTTTAAAAGA | 120 |
| ATAATAGTAA | GCACAAAGGC | CCTGTAGCAG | GAGGGAGCTG | ATTGTCCATA | GTTCAGACAG | 180 |
| CAAAGAAGCT | GATGATGCAG | GTTGGGGTCA | GACCGTGTTT | GACTACAGAT | AGGATGTAA | 240 |
| GGGTTTTGGC | TTTTTAGGTT | TTTGTTTTAA | TTCTAAAAGT | AATGGAAAAT | GTACTCCTTT | 300 |
| TGGTGGTGGT | CTGAGAGAAG | GTACATCATT | AGAATGACAT | TTTGAAAACA | ACACTCAGGC | 360 |
| TGCTCAGTAG | AGAATGGCTT | CAAAGGATTT | AAAAGCAGAA | GCAGAAGGAC | ATATTAGAGA | 420 |
| AGGATTGTAT | AGTTTTCTGG | TAAAAGATGA | CAGTGAATTG | TATGGGCGAT | GGATTAGCCG | 480 |
| TGGAAGGTGT | TGAGTATAAG | TGGTCTCCAG | CCAAACTCTA | TGGTTACTGG | AATAAGAGAG | 540 |
| TAGGAACCCCT | TCTCAGGCTT | TATCTTTATC | TATTCTTGTC | AACAGTATGT | ACATGTGTCC | 600 |
| CCCAGCCCCA | AATAACTGTA | CAGTTTAATG | ATGTTCACTC | TATACAGTTC | CCAGAATCCA | 660 |
| TTGGAAATTG | CTGTAACAGC | ATATCCTCAA | TGCCCATCAA | TTCTCCACGT | CCAACCTCTC | 720 |
| CATGGCCTCC | TCTGCCTCTG | CTGATCTGTG | AACTTCCCAA | GCCCCTTCCC | CTACCTGCTT | 780 |
| TTGATTGGCT | TTAACTTTTA | CAATATCTTC | ATTACTCCAA | GTTTGTTCAA | CATCCTTTTT | 840 |
| ATTTTTTTAA | ATCATAGATT | GATTTAGTTT | ATTCTCTTTG | CCATTTTTGA | ATCTCATTAT | 900 |
| TTCTGTTTCT | CCTTGTTTAT | TAGTGGCTCT | GTTTTCCCTC | AATTGCCTCT | TGCTTTTGAG | 960 |
| AAGCTCTTGT | GATTCTTTTA | GGGCCATTG | CCATTGATT | GGTTTGTCTT | CCTTTTCCCT | 1020 |
| ATAAGCTTTA | AATATGGCAT | TATAGTTTTA | TCCCCTTCC | TCTTCTTTAG | GTACAACCTGC | 1080 |
| AGACACTTTG | CTCTTCCAAG | GTTACTAAGC | AGTGTCTGAC | ACAATGTAGA | AGCTCAACAA | 1140 |
| ATATTGGTTA | AATTTATTTT | TTCTATTGAT | TGTTCAAGCT | TTGATGACAT | CACTTAAAAT | 1200 |
| GTTTCTTGTA | CACACCCTGT | TTTCTACTGA | TATATGTATG | TGTATGGCTA | CCTGAATCCA | 1260 |
| GGTTTCTTCT | AGGAATATAC | AGAAAGTAAT | TGATTTCTCT | GTGGATCTCT | AACAGTGACA | 1320 |
| AGAATTTTCA | CCTATGCCTG | TGAGAATACC | TTCAAAAGTA | TTGGGTGCTC | ATCATAAACA | 1380 |
| CACATCAGTT | TAACAAACTC | TTATGGATGC | ATTGACTTTC | CCAGTTAGTT | GCTAGATGAC | 1440 |
| TTCGGATGAT | TTGCATAATG | GGTCTCAGTT | TCCATATCTG | TTAAATGGCA | ATAATCAGAG | 1500 |
| AATTTTAAAA | AATTTAAGGA | CACCTGGAAA | GCTTGAAAGA | TCCCTAGAAA | GCATGTGTTT | 1560 |
| ATTCCACATA | GTGGGAACATA | TGCTAGATTTC | CCAAAGACAC | AAAGACAACT | AAGACAACTT | 1620 |

AGAATAAGAA GGAAAAGAGA ATGATTCGTT GCAATGATCC CCTTGAAGCT CCAGTTGAAA 1680
 GTCAGAGTAT TGCCCTGGAT TGGAAGTAGT CTCCAAACTG ACATCATTTT CTTTTTCGAA 1740
 CCATATCTGG CCTGTCTCTC TTGCCAGTTG CATATTAAAG GTAACAGATT TGAAAATGTT 1800
 TGGAATAAAA GCTCTAGTTA GGTGTGGTGG CACACACCTG CCATCCCAGC TACTGGAGAG 1860
 TCTGAGACTC GATGATTGTT TCAGCCCAAG AGTTGGAGGT TGTAGTGAGC TATGATGGCA 1920
 CCACTGCACT CCAGTCTGTG TGACAGAGCG AAGACCTTGT CTCTAAGGAA AAAAAAAAAA 1980
 AAA 1983

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Thr Val Asn Cys Met Gly Asp Gly Leu Ala Val Glu Gly Val Glu
 1 5 10 15
 Tyr Lys Trp Ser Pro Ala Lys Leu Tyr Gly Tyr Trp Asn Lys Arg Val
 20 25 30
 Gly Thr Leu Leu Arg Leu Tyr Leu Tyr Leu Phe Leu Ser Thr Val Cys
 35 40 45
 Thr Cys Val Pro Gln Pro Gln Ile Thr Val Gln Phe Asn Asp Val His
 50 55 60
 Ser Ile Gln Phe Pro Glu Ser Ile Gly Asn Cys Cys Asn Ser Ile Ser
 65 70 75 80
 Ser Met Pro Ile Asn Ser Pro Arg Pro Thr Ser Pro Trp Pro Pro Leu
 85 90 95
 Pro Leu Leu Ile Cys Glu Leu Pro Lys Pro Leu Pro Leu Pro Ala Phe
 100 105 110
 Asp Trp Leu
 115

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1046 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGGCTTAGTT AGGAGCTATG GCTAAACATC ATCCTGATTT GATCTTTTGC CGCAAGCAGG 60
CTGGTGTGTC CATCGGAAGA CTGTGTGAAA AATGTGATGG CAAGTGTGTG ATTTGTGACT 120
CCTATGTGCG TCCCTGCACT CTGGTGCGCA TATGTGATGA GTGTAACATAT GGATCTTACC 180
AGGGGCGCTG TGTGATCTGT GGAGGACCTG GGGTCTCTGA TGCCTATTAT TGTAAGGAGT 240
GCACCATCCA GGAGAAGGAC AGAGATGGCT GCCCAAAGAT TGTCAATCTG GGGAGCTCTA 300
AGACAGACCT CTTCTATGAA CGCAAAAAAT ACGGCTTCAA GAAGARGTGA TTGGTGGGTG 360
GCCCCCTTCCT CCCCCCAACA TCAGTCTGCT GCAGCTGCCA GAAAACATGC CTACTACTAC 420
CAGCAGAAAAG GGAGCAGAGC CCAGAGCATC ACCAGGAGTG CCTGCTAGTG TACTGGCAGC 480
TTGCCACCCC CTCCTCTCCC TTCACCCAGA CACGTGGTAG GGATGGAAAA GGATTCTTCA 540
CAGAGCACTC TGGCACACCA TATCGGAGAA AACTTGATAG ATTAGTTAAT GGTTTTTTCTT 600
GAATTCGAGA AGCATAGATC TGTTCTCCAT ATTGGTATGT TCTCCCTCAA CCAAGATCTT 660
CTAAAAAGAA ATAATATTTT AGTCTTCTGC TTGAGGAACT GACTGTGAAG CGACGCCCAG 720
TGAAAAACAT GTTCTTGAG CAGCTCTGGT GGCAGCTGTC CTTGAGGAAC CTTTGGTGTG 780
TGGTGGGAAG CTATCAGAAC AAGAAATGTA GGCATTTCCC GTTTTTTTGG GGGGGGGGGG 840
TGGGGGGGCA GGGCTCTGCC CTCTTGAAAG GCATTTACTT GTTTAACACT TGTCCAGCTA 900
CAGTGGGGTA CAGTAGCTGG CTATTCACAG GCATCATCAT AGCCCACTAG TCTCATATTA 960
TTTTCTTTT GAGAAATTGG AACTCTTTC TGTGCTATT ATATTAATAA AGTTGGTGTT 1020
TATTTTCTGG TAAAAA AAAA 1046

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Lys | His | His | Pro | Asp | Leu | Ile | Phe | Cys | Arg | Lys | Gln | Ala | Gly | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Val | Ala | Ile | Gly | Arg | Leu | Cys | Glu | Lys | Cys | Asp | Gly | Lys | Cys | Val | Ile | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Cys | Asp | Ser | Tyr | Val | Arg | Pro | Cys | Thr | Leu | Val | Arg | Ile | Cys | Asp | Glu | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Cys | Asn | Tyr | Gly | Ser | Tyr | Gln | Gly | Arg | Cys | Val | Ile | Cys | Gly | Gly | Pro | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Gly | Val | Ser | Asp | Ala | Tyr | Tyr | Cys | Lys | Glu | Cys | Thr | Ile | Gln | Glu | Lys | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Asp | Arg | Asp | Gly | Cys | Pro | Lys | Ile | Val | Asn | Leu | Gly | Ser | Ser | Lys | Thr | |
| | | | 85 | | | | | 90 | | | | | | 95 | | |
| Asp | Leu | Phe | Tyr | Glu | Arg | Lys | Lys | Tyr | Gly | Phe | Lys | Lys | Xaa | | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1814 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ATCTTGCACT | GGGCCTCTGT | CCCAAAAACA | AGCAGAATTT | TTTCTTTCTC | AACAGGCTTC | 60 |
| TTTGCTAAAG | AATGATGAGA | CTAAGGCCCT | CACTCCAGCT | TCCTTGCAAG | AGGAATTAAA | 120 |
| CAATTTGTTG | AAATTTAATC | CTGATTTTGC | TGAAGCGCAT | TATCTCAGCT | ACTTAAACAA | 180 |
| CCTCCGTGTC | CAAGATGTTT | TCAGTTCAAC | ACACAGTCTC | CTCCATTATT | TTGATCGTCT | 240 |
| GATTCTTACC | GGAGCCGAAA | GCAAAAGTAA | TGGGGAAGAR | GGCTATGGCC | GGAGCTTGAG | 300 |
| ATACGCCGCT | CTGAATCTTG | CCGCCCTGCA | CTGCCGCTTC | GGTCACTATC | AACAGGCAGA | 360 |
| GCTCGCCCTG | CAGGARGCAA | TTAGGATTGC | CCAGGARTCC | AACGATCACG | TGTGTCTCCA | 420 |
| GCACTGTTTG | AGCTGGCTTT | ATGTGCTGGG | GCAGAAGAGA | TCCGATAGCT | ATGTTCTGCT | 480 |
| GGAGCATTCT | GTGAAGAAGG | CAGTACATTT | TGGGTTACCG | TACCTCGCCT | CCCTGGGAAT | 540 |
| ACAGTCCCTT | GTTCAACAGA | GAGCTTTTGC | TGGGAAGACG | GCAAACAAGC | TGATGGATGC | 600 |

| | |
|--|------|
| CCTAAAGGAC TCCGACYTCC TGCCTGGAA ACACAGCCTG TCAGAGCTCA TCGATATCAG | 660 |
| CATCGCACAG AAAACGGCCA TCTGGAGGCT GTATGGCCGC AGCACCATGG CACTGCAACA | 720 |
| GGCCCAGATG TTGCTGAGCA TGAACAGCCT GGAGGCGGTG AATGCGGGCG TGCAGCAGAA | 780 |
| CAACACAGAG TCCTTTGCTG TCGCACTCTG CCACCTCGCA GAGCTACACG CGGAGCAGGG | 840 |
| CTGTTTTGCT GCAGCTTCTG AAGTGTTAAA GCACTTGAAG GAACGATTTC CGCCTAATAG | 900 |
| TCAGCACGCC CAGTTATGGA TGCTATGTGA TCAAAAATA CAGTTTGACA GAGCAATGAA | 960 |
| TGATGGCAAA TATCATTTGG CTGATTCCTG TGTTACAGGA ATCACAGCTC TCAATAGCAT | 1020 |
| AGAGGGTGTT TATAGGAAAG CGGTTGTATT ACAAGCTCAG AACCAAATGT CAGAGGCACA | 1080 |
| TAAGCTTTTA CAAAATTGT TGGTTCATTG TCAGAACTG AAGAACACAG AAATGGTGAT | 1140 |
| CAGTGTCCCTA CTGTCCGTGG CAGAGCTGTA CTGGCGATCT TCCTCCCCTA CCATCGCGCT | 1200 |
| GCCCATGCTC CTGCAGGCTC TGGCCCTCTC CAAGGAGTAC CGGTTACAGT ACTTGGCCTC | 1260 |
| TGAAACAGTG CTGAACTTGG CTTTTGCGCA GCTCATTCTT GGAATCCCAG AACAGGCCTT | 1320 |
| AAGTCTTCTC CACATGGCCA TCGAGCCCAT CTTGGCTGAC GGGGCTATCC TGGACAAAGG | 1380 |
| TCGTGCCATG TTCTTAGTGG CCAAGTGCCA GGTGGCTTCA GCAGCTTCCT ACGATCAGCC | 1440 |
| GAAGAAAGCA GAAGCTCTGG AGGCTGCCAT CGAGAACCTC AATGAAGCCA AGAACTATTT | 1500 |
| TGCAAAGGTT GACTGCAAAG AGCGCATCAG GGACGTCGTT TACTTCCAGG CCAGACTCTA | 1560 |
| CCATACCCTG GGGAAGACCC AGGAGAGGAA CCGGTGTGCG ATGCTCTTCC GGCAGCTGCA | 1620 |
| TCAGGAGCTG CCCTCTCATG GGGTACCCTT GATAAACCAT CTCTAGAGAG GACATCCCTG | 1680 |
| CTGGGCTGCT GTGCAGAGTA TAAGATTTTG GACTTGTTCA TGTCCCCTCT CTCCCTATAA | 1740 |
| ATGATGTATT TGTGACACCC TATCTTGTC AATAACAGCA TTCTGATTAG TTTGTCTTAA | 1800 |
| AAAAAAAAAA AAAA | 1814 |

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Asp Ala Leu Lys Asp Ser Asp Xaa Leu His Trp Lys His Ser Leu

| | | | |
|---|-----|-----|-----|
| 1 | 5 | 10 | 15 |
| Ser Glu Leu Ile Asp Ile Ser Ile Ala Gln Lys Thr Ala Ile Trp Arg | 20 | 25 | 30 |
| Leu Tyr Gly Arg Ser Thr Met Ala Leu Gln Gln Ala Gln Met Leu Leu | 35 | 40 | 45 |
| Ser Met Asn Ser Leu Glu Ala Val Asn Ala Gly Val Gln Gln Asn Asn | 50 | 55 | 60 |
| Thr Glu Ser Phe Ala Val Ala Leu Cys His Leu Ala Glu Leu His Ala | 65 | 70 | 75 |
| Glu Gln Gly Cys Phe Ala Ala Ala Ser Glu Val Leu Lys His Leu Lys | 85 | 90 | 95 |
| Glu Arg Phe Pro Pro Asn Ser Gln His Ala Gln Leu Trp Met Leu Cys | 100 | 105 | 110 |
| Asp Gln Lys Ile Gln Phe Asp Arg Ala Met Asn Asp Gly Lys Tyr His | 115 | 120 | 125 |
| Leu Ala Asp Ser Leu Val Thr Gly Ile Thr Ala Leu Asn Ser Ile Glu | 130 | 135 | 140 |
| Gly Val Tyr Arg Lys Ala Val Val Leu Gln Ala Gln Asn Gln Met Ser | 145 | 150 | 155 |
| Glu Ala His Lys Leu Leu Gln Lys Leu Leu Val His Cys Gln Lys Leu | 165 | 170 | 175 |
| Lys Asn Thr Glu Met Val Ile Ser Val Leu Leu Ser Val Ala Glu Leu | 180 | 185 | 190 |
| Tyr Trp Arg Ser Ser Ser Pro Thr Ile Ala Leu Pro Met Leu Leu Gln | 195 | 200 | 205 |
| Ala Leu Ala Leu Ser Lys Glu Tyr Arg Leu Gln Tyr Leu Ala Ser Glu | 210 | 215 | 220 |
| Thr Val Leu Asn Leu Ala Phe Ala Gln Leu Ile Leu Gly Ile Pro Glu | 225 | 230 | 235 |
| Gln Ala Leu Ser Leu Leu His Met Ala Ile Glu Pro Ile Leu Ala Asp | 245 | 250 | 255 |
| Gly Ala Ile Leu Asp Lys Gly Arg Ala Met Phe Leu Val Ala Lys Cys | 260 | 265 | 270 |
| Gln Val Ala Ser Ala Ala Ser Tyr Asp Gln Pro Lys Lys Ala Glu Ala | 275 | 280 | 285 |
| Leu Glu Ala Ala Ile Glu Asn Leu Asn Glu Ala Lys Asn Tyr Phe Ala | 290 | 295 | 300 |
| Lys Val Asp Cys Lys Glu Arg Ile Arg Asp Val Val Tyr Phe Gln Ala | | | |

Arg Leu Tyr His Thr Leu Gly Lys Thr Gln Glu Arg Asn Arg Cys Ala
325 330 335

Met Leu Phe Arg Gln Leu His Gln Glu Leu Pro Ser His Gly Val Pro
340 345 350

Leu Ile Asn His Leu
355

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:51:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| CAGAATGTCT | TAACATGAGA | ATTGAATTTT | ATGATGTTTG | GTTCCATTTA | ATAGCGGACA | 60 |
| CCACCCCAAT | CTCATGTTTT | CCTGTTACCC | TAAACAGTG | GAAGGAACT | GGGTGTTTGG | 120 |
| TAGACTTCTA | AATCATGGTC | TCTGACAATT | TGAATCTGAG | ATTCTCACCT | CCATTTACTA | 180 |
| AAGAATCGTG | ACTTAATTCA | AATTGCACAG | TAATCAGTAA | AGTGAATACG | TTTTTAAAAT | 240 |
| GGAATTTTCT | CCCTTCAGCA | AGCACTCATT | AAGGAGTGAG | GCTGAGTATT | TTAAGATAGA | 300 |
| GTGAGATCTG | TGAGTGATTG | AAAGGTGATA | TTTAAAACT | TGGATTTTCAT | TCCAGTGTCA | 360 |
| GGTTTGGGTT | TTAAGTTCCT | TTGGTCCAGG | GAAGGGTCCA | AGCAGCCACA | GTTGCCCTAA | 420 |
| ATCTCCATCA | TTAAGTCTTC | CAGCAAGGTT | AAGTGCAGTA | TGGAAGGAGA | AGGGGGAAGA | 480 |
| GGACGGTAAC | GGCCCCACAC | TCCAGGCTGA | GAAAGAGTAA | TTAGGAGGCC | TGAGGAGGGG | 540 |
| CCGAGGAAAG | GCTGTTGGGG | TGTGCTGGGG | TTGGTACCCG | AGCGCCTTCC | CCTCACCTCA | 600 |
| ACCAGAGAAG | AGCATCCGGT | TGCTTTTTTA | AGCTTTTAGC | CTGCCCTAGC | AAGGACAAAG | 660 |
| CATGTTAGAT | TAGAGATGCT | TCTGCTGATC | GCAGGGGTTC | TTATTTGAAA | ACATCTATGA | 720 |
| TGGGGGTGGG | GTGGGAGGAG | ACAGGTTGTG | GTTATGCAGG | AAAATCTTGT | CCTAAAAATA | 780 |
| TATGAGTTTG | GGGGTAAGGG | GTGGGATAGC | CAAGCAAAAT | CAGTAATTAT | TTTAAAATGA | 840 |
| ACATATGAAT | TTTTATTAA | TTTLAGTTAA | ATACAGATTT | TACAACGAGG | TCAGCATAAG | 900 |
| CCTAAATCTA | TATAGAGGGC | TAAGTCAGGC | ATTGCTTGT | TTATTTGTAG | ACTGGATTAA | 960 |

AAACAACCTG TCCTGTTTTG TCAGTTCCCA GCTTCTTCGT TTAGAATAAA TTAGACCAAA 1020
 AGAAGAAACG TGCTTGCTCTC TGTATACCCG CAGAATGAAG TTACTGTTGT TAAAACCGGA 1080
 TTTTTTCATT TTACTAGGTT CCGAAGAGTC CAGATGCTTG GTAGATGTTC AATACGTGAT 1140
 TTTTTTTTTA ATTGAATGTG TTCATTAAAA ATCCTCCTTA ACATTTCTAG AAAGACTTCT 1200
 TTCAATAAAT AATGGAATCT TAGAGGAAAA GTGGTTTTTTT AAAAGCTAGG GAACTCCTCC 1260
 ACTAAAAGTA ACCATTGGAA ACCTCGAATG AGGGCTAAAAG TTTTAATCAT AAGAGAAAAAG 1320
 GCAGCATAAT GAAATGTGTA CACATACATA GTCAGTGGTC CATTTTAGGA AGCCAGTGGC 1380
 GTCTGATAAA GAAATGTTAA GAGTAGTGAG GTTGAGGAAG GAAATTGTGG GGATTTGAAA 1440
 TATTCTCTTT ATGTTGTTTC TCTTCTGAGT CATGGTAAAA CAATAAATTA TCATCTCTAG 1500
 GTGGCAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1540

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Lys Leu Leu Leu Lys Pro Asp Phe Phe Ile Leu Leu Gly Ser
 1 5 10 15
 Glu Glu Ser Arg Cys Leu Val Asp Val Gln Tyr Val Ile Phe Phe Leu
 20 25 30
 Ile Glu Cys Val His Leu Lys Ser Ser Leu Thr Phe Leu Glu Arg Leu
 35 40 45
 Leu Ser Ile Asn Asn Gly Ile Leu Glu Glu Lys Trp Phe Phe Lys Ser
 50 55 60

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ANTGACGCCTT TAGCTAGTCC TTCTATCA

29

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TNCAACAGTAT CAACCAGAAG TGCCAATC

29

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GNAAACAGTAT TAAATTGCAG AGTTCCAG

29

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CNAATCATCAT CTCGCTTACA CAGTCAGG

29

- (2) INFORMATION FOR SEQ ID NO:57:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ANCGAGACAGA CCAAGGCTCA CAGGTGAA

29

- (2) INFORMATION FOR SEQ ID NO:58:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GNGGACACACA CTCATAAAAC AGAAAATA

29

- (2) INFORMATION FOR SEQ ID NO:59:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ANTAACCATAG AGTTTGGCTG GAGACCAC

29

- (2) INFORMATION FOR SEQ ID NO:60:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ANTCTTCCGAT GGCAACACCA GCCTGCTT

29

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GNTCACCATTT CTGTGTTCTT CAGTTTCT

29

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

ANATTTAGGCT TATGCTGACC TCGTTGTA

29

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

| | | | | | | | | | | | | | | | | | | | |
|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Asn | Ala | Ser | Tyr | Ser | Asp | Ser | Tyr | Leu | Glu | Gly | Ile | Leu | Leu | 1 | 5 | 10 | 15 |
| Lys | Gly | Val | Phe | Thr | Cys | Glu | Pro | Trp | Ser | Val | Ser | Val | Gly | Trp | Ser | 20 | 25 | 30 | |
| Thr | Ser | Val | Asp | Cys | Gly | Trp | Phe | Gln | Ser | Ala | Trp | Leu | Arg | Ser | Ser | 35 | 40 | 45 | |
| Thr | Glu | Gly | Ser | Thr | Gly | Ala | Ala | Leu | Trp | Gln | Arg | Leu | Arg | Arg | Glu | 50 | 55 | 60 | |
| Met | Asp | Gln | Pro | Thr | Pro | Gly | Thr | Trp | Leu | His | Gly | Ile | Arg | Lys | Gly | 65 | 70 | 75 | 80 |
| Arg | Cys | Trp | Pro | Leu | Cys | Ser | Cys | Cys | Leu | Phe | Leu | Phe | Leu | Phe | Ala | 85 | 90 | 95 | |
| Phe | Asp | Leu | Val | Ala | Thr | Asp | Arg | Val | Ala | Arg | Asp | Leu | Val | Phe | Ser | 100 | 105 | 110 | |
| Ser | Arg | His | Pro | Ser | Thr | Pro | Ala | Leu | Ser | Gln | Val | Ser | Cys | Cys | His | 115 | 120 | 125 | |
| Ala | Asn | Ala | Met | Ser | Thr | Leu | Ala | Pro | Arg | Pro | Lys | Ser | Val | Gln | Arg | 130 | 135 | 140 | |
| Trp | Pro | Thr | Xaa | Ser | Ser | His | Tyr | Ser | Leu | Asn | Ser | Met | Tyr | His | Leu | 145 | 150 | 155 | 160 |
| Pro Leu | | | | | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 83 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Leu | Val | Gly | Gly | Pro | Phe | Leu | Pro | Pro | Thr | Ser | Val | Cys | Cys | Ser | Cys | 1 | 5 | 10 | 15 |
| Gln | Lys | Thr | Cys | Leu | Leu | Leu | Pro | Ala | Glu | Arg | Glu | Gln | Ser | Pro | Glu | 20 | 25 | 30 | |

His His Gln Glu Cys Leu Leu Val Tyr Trp Gln Leu Ala Thr Pro Ser
 35 40 45
 Ser Pro Phe Thr Gln Thr Arg Gly Arg Asp Gly Lys Gly Phe Phe Thr
 50 55 60
 Glu His Ser Gly Thr Pro Tyr Arg Arg Lys Leu Asp Arg Leu Val Asn
 65 70 75 80
 Gly Phe Ser

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1521 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GTAACCTTCT TCTGCGCGGC TGCAGCTCGG GACTTCGGCC TGACCCAGCC CCCATGGCTT 60
 CAGAAGAGCT ACAGAAAGAT CTAGAAGAGG TAAAGGTGTT GCTGGAAAAG GCTACTAGGA 120
 AAAGAGTACG TGATGCCCTT ACAGCTGAAA AATCCAAGAT TGAGACAGAA ATCAAGAACA 180
 AGATGCAACA GAAATCACAG AAGAAAGCAG AACTTCTTGA TAATGAAAAA CCAGCTGCTG 240
 TGGTTGCTCC CATAACAACG GGCTATACGG TGAAAATCAG TAATTATGGA TGGGATCAGT 300
 CAGATAAGTT TGTGAAAATC TACATTACCT TAACTGGAGT TCATCAAGTT CCCACTGAGA 360
 ATGTGCAGGT GCATTTTACA GAGAGGTCAT TTGATCTTTT GGTAAAGAAT CTAAATGGGA 420
 AGAGTTACTC CATGATTGTG AACAACTCTT TGAAACCCAT CTCTGTGGAA GGCAGTTCAA 480
 AAAAAGTCAA GACTGATACA GTTCTTATAT TGTGTAGAAA GAAAGTGGAA AACACAAGGT 540
 GGGATTACCT GACCCAGGTT GAAAAGGAGT GCAAAGAAAA AGAGAAGCCC TCCTATGACA 600
 CTGAAACAGA TCCTAGTGAG GGATTGATGA ATGTTCTAAA GAAAATTTAT GAAGATGGAG 660
 ACGATGATAT GAAGCGAACC ATTAATAAAG CCTGGGTGGA ATCAAGAGAG AAGCAAGCCA 720
 AAGGAGACAC GGAATTTTGA GACTTTAAAG TCGTTTTGGG AACTGTGATG TGATGTGGAA 780
 ATACTGATGT TTCCAGTAAG GGAATATTGG TGAGCTGCAT ATATAAATTT GACAGATAGC 840
 TATTTACATA GCCTTCTAAG TAAAGGCAAT GAATTCTCCA TTTCCTACTG GAGGATTTAT 900
 TTAAATAAAA TATGCTTATT AAACACTCCT GCAAAGATGG TTTTATTAGT ACCCTGGTCA 960

TTTTGTTCAA GGAAGGGTTA TATTGCATTC TCACGTGAAA TATAAAAAGC AAGTCTTGCC 1020
 CAATAAAAC GCTACATTGT GTGTATTTTT TGTTCAGCTA AGAATTGGAA AAGTATTTGC 1080
 TTGCCTTTTA AGTTACTGAC ATCAGCTTCC ACCAGTGTA AAATTGAGTA AAACCTGAAG 1140
 TTTTGCATAA AATGCAAATC GGTGCCTGTG CTTGAAGGTT GCTGTAGAGC ATCTGACCCC 1200
 TTATTACCAC CTTAAGCAAT GTATATGCCA TGCATTACCA TGCAC TAATT CAATCACAGG 1260
 TGTTTCTATC TAGATTTAAA TATATTTGTC AATGAATGTG GAATAGAAAA TCTAACATG 1320
 ACAATAATAG ACATATCTTT GTATGGTACC AGTTAGTTTT GCCGTGGATC AGATGGTTTA 1380
 TAAAAGTAAT AACCATAAAG CAAAAAATAA TTTGAAAGCC CGTCTATTCC TATGCTCAAT 1440
 AAAGTTAAGT TTTTTTCAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1500
 AAAAAAAAAA AAAAAAAAAA A 1521

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Glu | Glu | Leu | Gln | Lys | Asp | Leu | Glu | Glu | Val | Lys | Val | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Glu | Lys | Ala | Thr | Arg | Lys | Arg | Val | Arg | Asp | Ala | Leu | Thr | Ala | Glu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Lys | Ser | Lys | Ile | Glu | Thr | Glu | Ile | Lys | Asn | Lys | Met | Gln | Gln | Lys | Ser |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Gln | Lys | Lys | Ala | Glu | Leu | Leu | Asp | Asn | Glu | Lys | Pro | Ala | Ala | Val | Val |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ala | Pro | Ile | Thr | Thr | Gly | Tyr | Thr | Val | Lys | Ile | Ser | Asn | Tyr | Gly | Trp |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Asp | Gln | Ser | Asp | Lys | Phe | Val | Lys | Ile | Tyr | Ile | Thr | Leu | Thr | Gly | Val |
| | | | 85 | | | | | 90 | | | | | | 95 | |
| His | Gln | Val | Pro | Thr | Glu | Asn | Val | Gln | Val | His | Phe | Thr | Glu | Arg | Ser |
| | | | 100 | | | | | 105 | | | | | | 110 | |

Phe Asp Leu Leu Val Lys Asn Leu Asn Gly Lys Ser Tyr Ser Met Ile
115 120 125

Val Asn Asn Leu Leu Lys Pro Ile Ser Val Glu Gly Ser Ser Lys Lys
130 135 140

Val Lys Thr Asp Thr Val Leu Ile Leu Cys Arg Lys Lys Val Glu Asn
145 150 155 160

Thr Arg Trp Asp Tyr Leu Thr Gln Val Glu Lys Glu Cys Lys Glu Lys
165 170 175

Glu Lys Pro Ser Tyr Asp Thr Glu Thr Asp Pro Ser Glu Gly Leu Met
180 185 190

Asn Val Leu Lys Lys Ile Tyr Glu Asp Gly Asp Asp Asp Met Lys Arg
195 200 205

Thr Ile Asn Lys Ala Trp Val Glu Ser Arg Glu Lys Gln Ala Lys Gly
210 215 220

Asp Thr Glu Phe
225

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

| | |
|---|-----|
| TGCGTCATGC AGTGCGCCGG AGGAACTGTG CTCTTTGAGG CCGACGCTAG GGGCCCGGAA | 60 |
| GGGAAACTGC GAGGCGAAGG TGACCGGGGA CCGAGCATTT CAGATCTGCT CGGTAGACCT | 120 |
| GGTGCACCAC CACCATGTTG GCTGCAAGGC TGGTGTGTCT CCGGACACTA CCTTCTAGGG | 180 |
| TTTTCACCC AGCTTTCACC AAGGCCTCCC CTGTTGTGAA GAATTCCATC ACGAAGAATC | 240 |
| AATGGCTGTT AACACCTAGC AGGGAATATG CCACCAAAAC AAGAATTGGG ATCCGGCGTG | 300 |
| GGAGAACTGG CCAAGAACTC AAAGAGGCAG CATTGGAACC ATCGATGGAA AAAATATTTA | 360 |
| AAATTGATCA GATGGGAAGA TGGTTTGTG CTGGAGGGGC TGCTGTTGGT CTTGGAGCAT | 420 |
| TGTGCTACTA TGGCTTGGGA CTGTCTAATG AGATTGGAGC TATTGAAAAG GCTGTAATTT | 480 |
| GGCCTCAGTA TGTCAAGGAT AGAATTCATT CCACCTATAT GTACTTAGCA GGGAGTATTG | 540 |
| GTTTAACAGC TTTGTCTGCC ATAGCAATCA GCAGAACGCC TGTTCATG AACTTCATGA | 600 |

TGAGAGGCTC TTGGGTGACA ATTGGTGTGA CCTTTGCAGC CATGGTTGGA GCTGGAATGC 660
 TGGTACGATC AATACCATAT GACCAGAGCC CAGGCCCAAA GCATCTTGCT TGGTTGCTAC 720
 ATTCTGGTGT GATGGGTGCA GTGGTGGCTC CTCTGACAAT ATTAGGGGGT CCTCTTCTCA 780
 TCAGAGCTGC ATGGTACACA GCTGGCATTG TGGGAGGCCT CTCCACTGTG GCCATGTGTG 840
 CGCCCAGTGA AAAGTTTCTG AACATGGGTG CACCCCTGGG AGTGGGCCTG GGTCTCGTCT 900
 TTGTGTCTC ATTGGGATCT ATGTTTCTTC CACCTACCAC CGTGGCTGGT GCCACTCTTT 960
 ACTCAGTGGC AATGTACGGT GGATTAGTTC TTTTCAGCAT GTTCCTTCTG TATGATACCC 1020
 AGAAAGTAAT CAAGCGTGCA GAAGTATCAC CAATGTATGG AGTTCAAAAA TATGATCCCA 1080
 TTAACGAT GCTGAGTATC TACATGGATA CATTAAATAT ATTTATGCGA GTTGCAACTA 1140
 TGCTGGCAAC TGGAGGCAAC AGAAAGAAAT GAAGTGACTC AGCTTCTGGC TTCTCTGCTA 1200
 CATCAAATAT CTTGTTTAAT GGGGCAGATA TGCATTAAAT AGTTTGTACA AGCAGCTTTC 1260
 GTTGAAGTTT AGAAGATAAG AAACATGTCA TCATATTTAA ATGTTCCGGT AATGTGATGC 1320
 CTCAGGTCTG CCTTTTTTTC TGGAGAATAA ATGCAGTAAT CCTCTCCCAA ATAAGCACAA 1380
 AAAAAAAAAA AAAA 1394

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Met Leu Ala Ala Arg Leu Val Cys Leu Arg Thr Leu Pro Ser Arg Val
 1 5 10 15
 Phe His Pro Ala Phe Thr Lys Ala Ser Pro Val Val Lys Asn Ser Ile
 20 25 30
 Thr Lys Asn Gln Trp Leu Leu Thr Pro Ser Arg Glu Tyr Ala Thr Lys
 35 40 45
 Thr Arg Ile Gly Ile Arg Arg Gly Arg Thr Gly Gln Glu Leu Lys Glu
 50 55 60
 Ala Ala Leu Glu Pro Ser Met Glu Lys Ile Phe Lys Ile Asp Gln Met

| 65 | 70 | 75 | 80 |
|---|-----|-----|-----|
| Gly Arg Trp Phe Val Ala Gly Gly Ala Ala Val Gly Leu Gly Ala Leu | 85 | 90 | 95 |
| Cys Tyr Tyr Gly Leu Gly Leu Ser Asn Glu Ile Gly Ala Ile Glu Lys | 100 | 105 | 110 |
| Ala Val Ile Trp Pro Gln Tyr Val Lys Asp Arg Ile His Ser Thr Tyr | 115 | 120 | 125 |
| Met Tyr Leu Ala Gly Ser Ile Gly Leu Thr Ala Leu Ser Ala Ile Ala | 130 | 135 | 140 |
| Ile Ser Arg Thr Pro Val Leu Met Asn Phe Met Met Arg Gly Ser Trp | 145 | 150 | 155 |
| Val Thr Ile Gly Val Thr Phe Ala Ala Met Val Gly Ala Gly Met Leu | 165 | 170 | 175 |
| Val Arg Ser Ile Pro Tyr Asp Gln Ser Pro Gly Pro Lys His Leu Ala | 180 | 185 | 190 |
| Trp Leu Leu His Ser Gly Val Met Gly Ala Val Val Ala Pro Leu Thr | 195 | 200 | 205 |
| Ile Leu Gly Gly Pro Leu Leu Ile Arg Ala Ala Trp Tyr Thr Ala Gly | 210 | 215 | 220 |
| Ile Val Gly Gly Leu Ser Thr Val Ala Met Cys Ala Pro Ser Glu Lys | 225 | 230 | 235 |
| Phe Leu Asn Met Gly Ala Pro Leu Gly Val Gly Leu Gly Leu Val Phe | 245 | 250 | 255 |
| Val Ser Ser Leu Gly Ser Met Phe Leu Pro Pro Thr Thr Val Ala Gly | 260 | 265 | 270 |
| Ala Thr Leu Tyr Ser Val Ala Met Tyr Gly Gly Leu Val Leu Phe Ser | 275 | 280 | 285 |
| Met Phe Leu Leu Tyr Asp Thr Gln Lys Val Ile Lys Arg Ala Glu Val | 290 | 295 | 300 |
| Ser Pro Met Tyr Gly Val Gln Lys Tyr Asp Pro Ile Asn Ser Met Leu | 305 | 310 | 315 |
| Ser Ile Tyr Met Asp Thr Leu Asn Ile Phe Met Arg Val Ala Thr Met | 325 | 330 | 335 |
| Leu Ala Thr Gly Gly Asn Arg Lys Lys | 340 | 345 | |

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1908 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

| | |
|--|------|
| GCTTTTTTTT TTTTTTTTGG TTGAGATGGG GTCTCGCCAT GTTTCACACA CTGATCTTGA | 60 |
| ACTCCTGGGC TCCAGGAATT CTCCTACTTT GGCCTCCCAA AGTGTGGGA ATATTGGCAT | 120 |
| GAACCACAGC ACCTGACTTG CATATTTGTG AATTCACCAA ATTGCTTTTT TTAAATTGAT | 180 |
| TTCTAATTTT ATTTTCATTGT TATGGGGAAC ATACTTTGTA TGGTTTCAAT GTTTTAAAAT | 240 |
| TAATTGAGAC TTGTTTTATG ACTTAGCATA TGGTCTGTGT TGAAGAAGGC TCCATGTACA | 300 |
| CTTGAGAATA ATATGTATAC TGTGGTTGTT GGGTGGATTT TCTATGTATG TTTARGTGAT | 360 |
| ATGGTTTTAT AGTGTGTGTT AARTCTCTA TTTCTTCTT TTTCTGCCA GTTTTATTTT | 420 |
| TGAAAGCATA CTGARGTCTC CAACTCARTG CCTTAGCCTC CTGAGCAGTT GGGACTACAG | 480 |
| GCATACGCCA CTACACCCAG CAATTTTTTT GTATTTTTCT GTAGAGACAG AGTTTCACCA | 540 |
| TGTTGCCTAG GCTGGTCTCA GATTCCTGGA CTCAAGTGAT CTCGATCCC GGCCTCTGCC | 600 |
| TCCCGGGGTG CTGGGATTGC AGGCATGAGC TACTATGCCT GGCAAATTTT ATTTTCTCTT | 660 |
| TTATTTTGTC ACATAATTAA AGCTACTCCA GAATTCCTT GATTTCTGCT TGCCTGGTAT | 720 |
| ATCTTTTTTC CATTTTTTAA CTGTCAGCCT TTTTGTGCC TGTAAATCTA AAGTATGTGT | 780 |
| TTCGTAGATA ATATGTAGCT GGATCATATT TTAAAAATAT TTATCTGCC AAGCTCTGTC | 840 |
| TTTTGATTGG AGTATTCTTT CATTTATGTT TGTAATTACT GATGAGGGGG GCACTAATGT | 900 |
| CTGCTGTTTT GCTATTTGTT TCCCATGTC TTATGTCTT ATTACTGACT TTTTATTAA | 960 |
| ACAACATTT TCTTGGGTAC CATTTTAAGT CCCTCTCCA CTCATTTTTT AATGTTTTTT | 1020 |
| TGTGTTTACT TTTGTTTTTA TTGTTTGCCC TGATATTAAA ATTAACATTT TACCTTGAAA | 1080 |
| TAGTTGGCTT CAGATTAATA TCAACTTAGT TTCAATAGCA TAGGAAATTT GCTTCACTAT | 1140 |
| ATTTCCATTT TCTCCCGTC CTTTGTGCTA TTATTACTAT ACCAATTAGA TCTCTACACA | 1200 |
| ATATAGGCAT ATCAACACAT TTTGTAATTA TTTCTTATC CAGTTGTCTT TTAATATAGA | 1260 |
| TCTGTGAAGA AAAGTATTAC ACAAATAGAT CTATTCTGTT TTTTATAATT ATTTAATTAC | 1320 |
| CTTTGGTGGT GCTGTTTATT TTTCATGCAT TTGAGTTACT GTCTAGTATT CATTCATTTT | 1380 |
| TCTCTGAATC ACTCCCTTTA GTATTGCTTG TAGGGCAGGT CTGCTAGCAT TGAATCTTTT | 1440 |

TAATTTTGT GACTCTGCAA ATGCCATAAT TTCTCTTTTG TTTGTGAAGG ATAGTTTTC 1500
TAGATACAGA ATTTGCAGTT GGCATTCTTT TTTACTTTAGC AGTTTGAAAA TATTTCCCAT 1560
TGTTGGCCGG GCACAGTGGC TCACGCCTGT GGTCTAGCA CTTTGGGAGG CCGAGGCGGG 1620
CGGATCGTCT GGGGTCGGGA GTTCGGGACC GGCCTGGCCA ATATGGTGAG GCCCTGTTTC 1680
TGCTAAAATA TAAAAATTGG CTGGGCATGA TGGCGGGTGC CTCTAGTCCC AGCTGCTCGG 1740
GAGGCTGAGG TGGGGGAGTC GCTTGAGCCC GGGAGATGAT GGCTGTGGTG AGCCGGGATG 1800
GCGCCGCTGC ACTCCGGCCT GGGCGGCTGA GTGAGACTCC ATCCCCGAAA AAAAAAAAAA 1860
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAA 1908

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Gly | Ala | Leu | Met | Ser | Ala | Val | Leu | Leu | Phe | Val | Ser | Pro | Cys |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Met | Ser | Ser | Leu | Leu | Thr | Phe | Leu | Leu | Asn | Asn | Tyr | Phe | Leu | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Tyr | His | Phe | Lys | Ser | Leu | Ser | His | Ser | Phe | Phe | Asn | Val | Phe | Leu | Cys |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Leu | Leu | Phe | Leu | Leu | Phe | Ala | Leu | Ile | Leu | Lys | Leu | Thr | Phe | Tyr |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Leu | Glu | Ile | Val | Gly | Phe | Arg | Leu | Ile | Ser | Thr | | | | | |
| 65 | | | | | 70 | | | | | 75 | | | | | |

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3076 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CTTTTTTTTT TTTTTC AAT TTCATTTAGT TCTGCCCTGA TCTTGGTTAT TTCCTTTTTT 60
TCTGCTGGGT TTGGGTTTGG TTTGTTCTTA TTTCTCTAGT TCCTTGAGGT GTGACCTTAR 120
AATGTCAATT TGTGCTCTTT CAATCTTTTT GATGTAGGCG TTGAGGGCTG TGGACTTTTC 180
TCTTGGCACT CCCTTTGGTG TATCCCARAG GTTTTGATAG GTTGTGTCAT TATTGCAATT 240
CAGTTTGAAG AATTTCTTAA TCTCCACCTT GATTTTGTTT TTGACCCAAT GCTCATTCAG 300
GAGCAGGTTA TTTACTTTCC ATGTACTTGC ATGGCTTTGA AGCTTCCTTT TGGAGTTGAT 360
TTCCAGTTTT ATTCCACTGT GATTTGAGAG AGTGCTTTAC ATAATTTCAA TTTTCTTAAT 420
TTTATTAAGG CTCGTTTTAT GGCCTATAAT ATGGTCTATC TTGGAGAAAAG TTCCATGCAC 480
TGTAAGAATAG AATGTGTATT CTGTGGTTGT TGGATGAAAT GTTCTGCATA TATTCCTAGA 540
TTGCCTCCCC ACAAAGGTT GCATCAATGT CTGTGTTTCT CTACACCATC TCACCCTTGC 600
CAACTTCGGG TTTTCATCAGA CCTTACTGAT TGTCAGTATG ATCTGTGAAA CAAATCTCTC 660
AGTTTTGATT TGCATTTTTT AAATTATGAG AGCTTGAACA CCATTTTACA TGTTTATTGG 720
CTGTTGTTAT TTCCTTTTTG AGATCTGTTC GTTATATGCT TTGCCCCTTT TTCTGTTGGG 780
TGGTTATTAT TTTTCTTATT GAATGGTATA AGCTCTTTGT AAGTTAAGGA CATTAGCCCT 840
TAGTCAGATA TTTTGACTTA GGTTTTAATT TTTTCCACA CAGAAGTTTT AAGCTCTGTG 900
GCAAATTTAT CAGTCTTATA TCACTACAGG GTTATAAATA TTAGYTATCA CTTCGGGTTT 960
GTGTCTTGCT TAGAAAGCMT CATTTGAAGA TTGTAAATGT TAGTAAGTTT CCCCATATTT 1020
TCCTCTAGGA CTTCCATGGT TTAATTTGTT TTGTTTAAAY TAGGAATTGG CATTACATC 1080
CTYTTTTGTC CCAGGTCTCA GAGGTCCCTT GTATCTTATA GAGCAGTATT GTTTTATGTT 1140
ATTTTCCCAT GTATAATTTA AAAACAAAAT ACGTTGTTCA AAACAAAATA CAGTGGCAGC 1200
AGATAATGGC AGTATCTCTG TAACTGCTGG TAAACTGTAT TTCATAGTGA AGTGTTTATA 1260
AACTAAAGAG TCATTGATTT GGTTCCTGG CTAATTAAAA TCTGAATTCC ATTTGAAGTT 1320
CCATTGAAAT CATGGTTTTA CTCTATAGCA GTGGATGTTT TTTCCCAACC TTTCTGATAT 1380
TTTTTTCCTT CCTGAGACAG GGTCTTGCTC TGTCACCTGG GATGGAGTGT AGTTGCACCA 1440
TCAAGGCTTA CTGCAGTCTC AACTCTCTGA GCTCAAGTGA TCCTGCCACC TCAGCCTCTT 1500
GAGTAGCAAG GATTACAGGC ACCTACCACT ATGCCTGGCT AATTTTATA TTTTGTAG 1560
AGATGGATTC TCACTATGTT GCCC GGCTC ATCTTGAAC CGAGCTCAAG CAATCTGTCC 1620

| | |
|---|------|
| ATCTTGGCCT CCCAAAGTGC TGGGATTATA GGCGTGAGCC ACTGCACCTG GCCCCTTTCT | 1680 |
| GATTATTTTA ATCTATCTTT AAATGTTCAA AGTGATTGTC CTAATTCATT TAAAGCATAT | 1740 |
| TTAGTTTTTT TTAAATTGAG TGTATTTTAT CTAGATATTT TAAAAAGGCA GCATCTAACC | 1800 |
| TTGGATTTTA TAAATACATC TAAATTTGTT ATTTCCAGAA TGCTTCAAAA CAGATCTCTG | 1860 |
| TAGCCTCGTG CTTTGTTATT GTTAGGTTTT TTTTTTTTGT TTTGAGACAG GGTCTTGCTC | 1920 |
| TATCTGGAGT GCAGTGGCAC AGTCATAGCT CACTGTACCC TCAAACCTCT AAACCTCAAGT | 1980 |
| AATCCTCCCA TCTCAGCCTC CTGAGTAGTT GGGACCACAG TCATGCACCA GCATGCCTGG | 2040 |
| CTAATTTTTT AAATTTTGTT CTTAATAGAG ACAGAGTCTT GCTGTGTTGT TCAGGCTGGT | 2100 |
| CTCAAACCTC TGGGCTCAAG CGATCCTCCC ACCTCAGCCT CCTAAAGTGC TGAGATTACG | 2160 |
| GATGTGAATC ATTACACCCA GCCTATTAAT GGTTTTGTAT AGCAAGTCTT TTGTGGGTGG | 2220 |
| TGGAAAGATG AAGTGCTGTG AAATATTGTA GGAGCAGAAA CTTGAAATGT GGCAAAAACC | 2280 |
| ACATGGGCAA AATTTCTGTC TCTTTTCTTA TTTTGTCTTT TTTGTTTAAA GGTTTTTCTA | 2340 |
| TTGGGAAAGC TACTGATCGG ATGGATGCTT TCAGGAAAGC AAAGAACAGA GCAGTTCACC | 2400 |
| ATTTGCATTA TATAGAACGA TATGAAGACC ATACAATATT CCATGATATT TCATTAAGAT | 2460 |
| TTAAAAAGGAC GCATATCAAG ATGAAGAAAC AACCCTAAAGG TTACGGCCTC CGCTGCCACA | 2520 |
| GGGCCATCAT CACCATCTGC CGGCTCATTG GCATCAAAGA CATGTATGCC AAGGTCTCTG | 2580 |
| GGTCCATTAA TATGCTCAGC CTCACCCAGG GCCTCTTCCG TGGGCTCTCC AGACAGGAAA | 2640 |
| CCCATCAACA GCTGGCTGAT AAGAAGGGCC TCCATGTTGT GGAAATCCGG GAGGAATGTG | 2700 |
| GCCCTCTGCC CATTGTGGTT GCGTCCCCC GGGGGCCCTT GAGGAAGGAT CCAGAGCCAG | 2760 |
| AAGATGAGGT TCCAGACGTC AAACCTGGACT GGAAGATGT GAAGACTGCA CAGGGAATGA | 2820 |
| AGCGCTCTGT GTGGTCTAAT TTGAAGAGAG CCGCCACGTA ACCTCTCTGG CCTTGTGCAG | 2880 |
| CCAGTTCCTG TGCTGCCCTG CACCTAGGAG AGACTCAGCC CCTCACAGCT TGGGATGTTA | 2940 |
| CCTTGCCTTT TGTTTGTTTT GAGGGAAGTT TAATCTTTAA ACTCTTTGGA AATAAATAAT | 3000 |
| TATAGCTTTC AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA | 3060 |
| AAAAAAAAAA AAAAAA | 3076 |

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Lys | Ile | Ser | Val | Ser | Phe | Leu | Ile | Phe | Ala | Phe | Leu | Phe | Lys | 1 | 5 | 10 | 15 |
| Gly | Phe | Ser | Ile | Gly | Lys | Ala | Thr | Asp | Arg | Met | Asp | Ala | Phe | Arg | Lys | 20 | 25 | 30 | |
| Ala | Lys | Asn | Arg | Ala | Val | His | His | Leu | His | Tyr | Ile | Glu | Arg | Tyr | Glu | 35 | 40 | 45 | |
| Asp | His | Thr | Ile | Phe | His | Asp | Ile | Ser | Leu | Arg | Phe | Lys | Arg | Thr | His | 50 | 55 | 60 | |
| Ile | Lys | Met | Lys | Lys | Gln | Pro | Lys | Gly | Tyr | Gly | Leu | Arg | Cys | His | Arg | 65 | 70 | 75 | 80 |
| Ala | Ile | Ile | Thr | Ile | Cys | Arg | Leu | Ile | Gly | Ile | Lys | Asp | Met | Tyr | Ala | 85 | 90 | 95 | |
| Lys | Val | Ser | Gly | Ser | Ile | Asn | Met | Leu | Ser | Leu | Thr | Gln | Gly | Leu | Phe | 100 | 105 | 110 | |
| Arg | Gly | Leu | Ser | Arg | Gln | Glu | Thr | His | Gln | Gln | Leu | Ala | Asp | Lys | Lys | 115 | 120 | 125 | |
| Gly | Leu | His | Val | Val | Glu | Ile | Arg | Glu | Glu | Cys | Gly | Pro | Leu | Pro | Ile | 130 | 135 | 140 | |
| Val | Val | Ala | Ser | Pro | Arg | Gly | Pro | Leu | Arg | Lys | Asp | Pro | Glu | Pro | Glu | 145 | 150 | 155 | 160 |
| Asp | Glu | Val | Pro | Asp | Val | Lys | Leu | Asp | Trp | Glu | Asp | Val | Lys | Thr | Ala | 165 | 170 | 175 | |
| Gln | Gly | Met | Lys | Arg | Ser | Val | Trp | Ser | Asn | Leu | Lys | Arg | Ala | Ala | Thr | 180 | 185 | 190 | |

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 683 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

| | |
|---|-----|
| CGCCAAGTGC GCATGGGGAC GCTATAGCAA TTCGTTTGCT GTCCTTCCTC TCCTTCGAAG | 60 |
| ATGACAAGGC CTACCATCGT TTCTTCCTGC CTTTGGGCCG TCAGGCAGTT GGTGGGACC | 120 |
| CGCTCCAACC CTCGGTTCTT CCTGCAATAC AGTGGATACA ATTTGTCATG GCTACTCTGA | 180 |
| GTGTTATAGG TTCAAGTTCA CTTATTGCCT ATGCTGTATT CCATAATATA CAGAAATCTC | 240 |
| CAGAGATAAG ACCACTTTTT TATCTGAGCT TCTGTGACCT GCTCCTGGGA CTTTGCTGGC | 300 |
| TCACGGAGAC ACTTCTCTAT GGAGCTTCAG TAGCAAATAA GGACATCATC TGCTATAACC | 360 |
| TACAAGCAGT TGGACAGATA TTCTACATTT CCTCATTTCT CTACACCGTC AATTACATCT | 420 |
| GGTATTTGTA CACAGAGCTG AGGATGAAAC ACACCCAGAG TGGACAGAGC ACATCTCCAC | 480 |
| TGGTGATAGA TTATACTTGT CGAGTTGGTC AAATGGCCTT TGTTTTCTCA AGCCTGATAC | 540 |
| CTCTGCTATT GATGACACCT GTATTCTGTC TGGGAAATAC TAGTGAATGT TTCCAAAAC | 600 |
| TCAGTCAGAG CCACAAGTGT ATCTTGATGC ACTCACCACC ATCAGCCATG GCTGAACTTC | 660 |
| CACCTTCTGC CAACACATCT GTC | 683 |

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Thr | Leu | Ser | Val | Ile | Gly | Ser | Ser | Ser | Leu | Ile | Ala | Tyr | Ala |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Val | Phe | His | Asn | Ile | Gln | Lys | Ser | Pro | Glu | Ile | Arg | Pro | Leu | Phe | Tyr |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Ser | Phe | Cys | Asp | Leu | Leu | Leu | Gly | Leu | Cys | Trp | Leu | Thr | Glu | Thr |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Leu | Tyr | Gly | Ala | Ser | Val | Ala | Asn | Lys | Asp | Ile | Ile | Cys | Tyr | Asn |
| | 50 | | | | | 55 | | | | 60 | | | | | |
| Leu | Gln | Ala | Val | Gly | Gln | Ile | Phe | Tyr | Ile | Ser | Ser | Phe | Leu | Tyr | Thr |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Val | Asn | Tyr | Ile | Trp | Tyr | Leu | Tyr | Thr | Glu | Leu | Arg | Met | Lys | His | Thr |

| | | | |
|---|-----|-----|-----|
| | 85 | 90 | 95 |
| Gln Ser Gly Gln Ser Thr Ser Pro Leu Val Ile Asp Tyr Thr Cys Arg | | | |
| | 100 | 105 | 110 |
| Val Gly Gln Met Ala Phe Val Phe Ser Ser Leu Ile Pro Leu Leu Leu | | | |
| | 115 | 120 | 125 |
| Met Thr Pro Val Phe Cys Leu Gly Asn Thr Ser Glu Cys Phe Gln Asn | | | |
| | 130 | 135 | 140 |
| Phe Ser Gln Ser His Lys Cys Ile Leu Met His Ser Pro Pro Ser Ala | | | |
| | 145 | 150 | 155 |
| | | | 160 |
| Met Ala Glu Leu Pro Pro Ser Ala Asn Thr Ser Val | | | |
| | 165 | 170 | |

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

| | |
|---|-----|
| ATATGGCTGG ACGCAGCACA AATTCCACCA ACTAAAGCAG GAGGCTCGGC GTGATGCAGA | 60 |
| TACCCAGACA CCATTATTAT GCTCACAGAA GAGATTCTAT AGCAGGGGCT TAAATTCCT | 120 |
| GGAATCCACC CTGACTTTTC CTGCCAGTAC TTCTACCATT TTTTGAAACT ACAATACTGG | 180 |
| AACATCCAGG AACTGGAGTT ATTCTACGCT AATGGATTGG AAAGAATGTT GGGAAAGGAC | 240 |
| ATCTTAAATC TTTTCTAACT ATGCCCTAAA CTGCAGAACT CAAAGGAAAT ATAGTGCCAT | 300 |
| TGTTAGTAGT CATTCTAGAT GAATTGGGAG TATCTCTCCA GTTATTCCCA GATTCCTAG | 360 |
| TGATCCTTAA AGTCTCTATT CAGGGAGAGG AAGACACTTT CCATCTCAGA GATAGACTCG | 420 |
| TGTTACCTTG ATGGATATTG GATTTGTCTA AGTCTCTTCT AGAAAAAATA AATTCTAGAT | 480 |
| TATTAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA | 524 |

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

| | |
|--|------|
| CCCCGCTACC GGGTTGCGGC CGGAAGCCGG GCGCCGCGGC TCTGCTTCCC TCGGGGATCT | 60 |
| GGCGACATGG CCAGAAAGGC TCTCAAGCTT GCTTCGTGGA CCAGCATGGC TCTTGCTGCC | 120 |
| TCTGGCATCT ACTTCTACAG TAACAAGTAC TTGGACCCTA ATGACTTTGG CGCTGTCAGG | 180 |
| GTGGGCAGAG CAGTTGCTAC GACGGCTGTC ATCAGTTACG ACTACCTCAC TTCCCTGAAG | 240 |
| AGTGTCCTT ATGGCTCAGA GGAGTACTTG CAGCTGAGAT CTAAGGTGCA CCTTCGCTCT | 300 |
| GCCAGGCGTC TCTGTGAGCT CTGCTGTGCC AACCGGGGCA CCTTCATCAA GGTGGGCCAG | 360 |
| CACCTGGGGG CTCTGGACTA CCTGTTGCCA GAGGAGTACA CCAGCACGCT GAAGGTACTG | 420 |
| CACAGCCAGG CTCCACAGAG CAGCATGCAA GAGATCCGCC AGGTCATCCG AGAAGATCTG | 480 |
| GGCAAGGAGG TGCTCGTTCT GGCTGTGAAG CAGCTGTTCC CAGAGTTTGA GTTTATGTGG | 540 |
| CTTGTTGGATG AAGCCAAGAA GAACCTGCCT TTGGAGCTGG ATTTCTCAA TGAAGGGAGG | 600 |
| AATGCTGAGA AGGTGTCCCA GATGCTCAGG CATTTTGA CTCTGAAGGT CCCCCGAATC | 660 |
| CACTGGGACC TGTCCACGGA GCGGGTCCTC CTGATGGAGT TTGTGGATGG CGGGCAGGTC | 720 |
| AATGACAGAG ACTACATGGA GAGGAACAAG ATCGACGTCA ATGAGGTGAG GTCAAGAGCT | 780 |
| CAGGGCTGCT GTGCCGGGGA ACGTGGGCTT GGTCAAGGCT GCCCAGGAAG TGCCTGTGTG | 840 |
| TCCAGATCTC ACGCCACCTG GGCAAGATGT ATAGTGAGAT GATCTTCGTC AATGGCTTCG | 900 |
| TGCACTGCGA TCCCCACCCC GGCAATGTAC TGGTGCGGAA GCACCCCGGC ACGGGAAAAGG | 960 |
| CGGAGATTGT CCTGTTGGAC CATGGGCTTT ACCAGATGCT CACGGAAGAA TTCCGCCTGA | 1020 |
| ATTACTGCCA CCTCTGGCAG TCTCTGATCT GGA CTGACAG GAAGAGAGTG AAGGAGTACA | 1080 |
| GCCAGCGACT GGGAGCCGGG GATCTCTACC CCTTGTTTGC CTGCATGCTG ACGGCGCGAT | 1140 |
| CGTGGGACTC GGTCAACAGA GGCATCAGCC AAGCTCCCGT CACTGCCACT GAGGACTTAG | 1200 |
| AGATTGCGAA CAACGCGGCC AACTACCTCC CCCAGATCAG CCATCTCCTC AACCACGTGC | 1260 |
| CGCGCCAGAT GCTGCTCATC TTGAAGACCA ACGACCTGCT GCGTGGCATT GAGGCCGCCC | 1320 |
| TGGGCACCCG CGCCAGCGCC AGCTCCTTTC TCAACATGTC ACGTTGCTGC ATCAGAGCGC | 1380 |
| TAGCTGAGCA CAAGAAGAAG AATACCTGTT CATCTTTCAG AAGGACCCAG ATCTCTTTCA | 1440 |
| GCGAGGCCTT CAACTTATGG CAGATCAACC TCCATGAGCT CATCCTGCGT GTGAAGGGGT | 1500 |
| TGAAGCTGGC TGACCGGGTC TTGGCCCTAA TATGCTGGCT GTTCCCTGCT CCACTCTGAG | 1560 |

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TGGAATTGCT CTCCCTGCCC CATTCTGGTG TCTTTCCACT CCTCAGCCCC TCATCTTGCC      1620
TCCACCCAGC TGCTCCATTT TTGCCACATC GTGGCCCGCA GCCCAGAGT CACTGTCCAT      1680
GTCACCATCC TCCTCCTCCT TTGGAATCCT CTCCGCACAC TGTGGCCCTT GTCTCAGGGC      1740
CCACAAGCTG AACTGTGGCA TAGCTCTCTC TTCTTCTCCA AGAAGACTCA GCAGCCTACA      1800
TTCCCATTC TGGTATGTGC CATTGGGTTG GATGTCCCCA CTAATTCCGT TAACCCTTCC      1860
CATTGTCAAG ATGTGCCACG GGTGCCACTG GGGGCACACT GAACTTGTAG GGAGTGTGAT      1920
TTTGTGGAG GTGCACATGG TCTCTGAATT TGACAGAGAA CACCTTCCCT TTCCTTGCCA      1980
TGTCACCCTC CAGAGGAAGT CACACCTCAG CGAGGTGGTT TGGCATCTGG GGCCAACTCC      2040
ATTACAGCTA TGAGCTCACT GCTGTCAGTG ACGTTTGGTG TTTTCTGTAC TGTGTTTCAA      2100
TAAAAACTCC TTCAAGGTTG CAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA      2160
AAAAAAAAAA A                                                    2171

```

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```

Met Ala Arg Lys Ala Leu Lys Leu Ala Ser Trp Thr Ser Met Ala Leu
1           5           10           15
Ala Ala Ser Gly Ile Tyr Phe Tyr Ser Asn Lys Tyr Leu Asp Pro Asn
20          25          30
Asp Phe Gly Ala Val Arg Val Gly Arg Ala Val Ala Thr Thr Ala Val
35          40          45
Ile Ser Tyr Asp Tyr Leu Thr Ser Leu Lys Ser Val Pro Tyr Gly Ser
50          55          60
Glu Glu Tyr Leu Gln Leu Arg Ser Lys Val His Leu Arg Ser Ala Arg
65          70          75          80
Arg Leu Cys Glu Leu Cys Cys Ala Asn Arg Gly Thr Phe Ile Lys Val
85          90          95
Gly Gln His Leu Gly Ala Leu Asp Tyr Leu Leu Pro Glu Glu Tyr Thr
100         105         110

```

Ser Thr Leu Lys Val Leu His Ser Gln Ala Pro Gln Ser Ser Met Gln
115 120 125

Glu Ile Arg Gln Val Ile Arg Glu Asp Leu Gly Lys Glu Val Leu Val
130 135 140

Leu Ala Val Lys Gln Leu Phe Pro Glu Phe Glu Phe Met Trp Leu Val
145 150 155 160

Asp Glu Ala Lys Lys Asn Leu Pro Leu Glu Leu Asp Phe Leu Asn Glu
165 170 175

Gly Arg Asn Ala Glu Lys Val Ser Gln Met Leu Arg His Phe Asp Phe
180 185 190

Leu Lys Val Pro Arg Ile His Trp Asp Leu Ser Thr Glu Arg Val Leu
195 200 205

Leu Met Glu Phe Val Asp Gly Gly Gln Val Asn Asp Arg Asp Tyr Met
210 215 220

Glu Arg Asn Lys Ile Asp Val Asn Glu Val Arg Ser Arg Ala Gln Gly
225 230 235 240

Cys Cys Ala Gly Glu Arg Gly Leu Gly Gln Gly Cys Pro Gly Ser Ala
245 250 255

Cys Val Ser Arg Ser His Ala Thr Trp Ala Arg Cys Ile Val Arg
260 265 270

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1613 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CATGGCGGCT CCCTTGGTCC TGGTGCTGGT GGTGGCTGTG ACAGTGC GGG CGGCCTTGTT 60

CCGCTCCAGT CTGGCCGAGT TCATTTCCGA GCGGGTGGAG GTGGTGTCCC CACTGAGCTC 120

TTGGAAGAGA GTGGTTGAAG GCCTTTCACT GTTGGACTTG GGAGTATCTC CGTATTCTGG 180

AGCAGTATTT CATGAACTC CATTAATAAT ATACCTCTTT CATTTCCTAA TTGACTATGC 240

TGAATTGGTG TTTATGATAA CTGATGCACT CACTGCTATT GCCCTGTATT TTGCAATCCA 300

GGACTTCAAT AAAGTTGTGT TTAAAAAGCA GAAACTCCTC CTAGAACTGG AACAGTATGC 360

| | |
|--|------|
| CCCAGATGTG GCCGAACTCA TCCGGACCCC TATGGAAATG CGTTACATCC CTTTGAAAGT | 420 |
| GGCCCTGTTC TATCTCTTAA ATCCTTACAC GATTTTGTCT TGTGTTGCCA AGTCTACCTG | 480 |
| TGCCATCAAC AACACCCTCA TTGCTTTCTT CATTTTGA CT ACATAAAAAG TTTCATTATC | 540 |
| TGTAAATGG GGACAGTAAT TGTACCCACT TCATGGAATT ATTGAGAAGA CTAAATGGCT | 600 |
| TAAGGCAGTG CTTTCCTCAG TGCTATTTTT CTTGCCTTAG CGACATACCA GTCTCTGAAC | 660 |
| CCACTCACCT TGTTCGTCCC AGGACTCCTC TATCTCCTCC AGCGGCAGTA CATACTGTG | 720 |
| AAAAATGAAGA GCAAAGCCTT CTGGATCTTT TCTTGGGAGT ATGCCATGAT GTATGTGGGA | 780 |
| AGCCTAGTGG TAATCATTTG CCTCTCCTTC TTCCTTCTCA GCTCTTGGGA TTTCATCCCC | 840 |
| GCAGTCTATG GCTTTATACT TTCTGTTCCA GATCTCACTC CAAACATTGG TCTTTTCTGG | 900 |
| TACTTCTTGG CAGAGATGTT TGAGCACTTC AGCCTCTTCT TTGTATGTGT GTTTCAGATC | 960 |
| AACGTCTTCT TCTACACCAT CCCCTTAGCC ATAAAGCTAA ATCCTGAGAA ACATCTTTGT | 1020 |
| CCTCACCTGC ATCATCATCG TCTGTTCCCT GCTCTTCCCT GTCCTGTGGC ACCTCTGGAT | 1080 |
| TTATGCAGGA AGTGCCAACT CTAATTTCTT TTATGCCATC AACTGACCT TCAACGTTGG | 1140 |
| GCAGATCCTG CTCATCTCTG ATTACTTCTA TGCCTTCCTG CGGCGGGAGT ACTACCTCAC | 1200 |
| ACATGGCCTC TACTTGACCG CCAAGGATGG CACAGAGGCC ATGCTCGTGC TCAAGTAGGC | 1260 |
| CTGGCTGGCA CAGGGCTGCA TGGACCTCAG GGGGCTGTGG GGCCAGAAGY TGGGCCAAGC | 1320 |
| CCTCCAGCCA GAGTTGCCAG CAGGCGAGTG CTTGGGCAGA AGAGGTTCTGA GTCCAGGGTC | 1380 |
| ACAAGTCTCT GGTACCAAAA GGGACCCATG GCTGACTGAC AGCAAGGCCT ATGGGGAAGA | 1440 |
| ACTGGGAGYT CCCCAACTTG GACCCCCACC TTGTGGCTCT GCACACCAAG GAGCCCCYTC | 1500 |
| CCAGACAGGA AGGAGAAGAG GCAGGTGAGC AGGGCTTGTT AGATTGTGGC TACTTAATAA | 1560 |
| ATGTTTTTTT TTATGAAGTC TAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA | 1613 |

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Ala Ala Pro Leu Val Leu Val Leu Val Val Ala Val Thr Val Arg

| | | | |
|---|-----|-----|-----|
| 1 | 5 | 10 | 15 |
| Ala Ala Leu Phe Arg Ser Ser Leu Ala Glu Phe Ile Ser Glu Arg Val | | | |
| 20 | 25 | 30 | |
| Glu Val Val Ser Pro Leu Ser Ser Trp Lys Arg Val Val Glu Gly Leu | | | |
| 35 | 40 | 45 | |
| Ser Leu Leu Asp Leu Gly Val Ser Pro Tyr Ser Gly Ala Val Phe His | | | |
| 50 | 55 | 60 | |
| Glu Thr Pro Leu Ile Ile Tyr Leu Phe His Phe Leu Ile Asp Tyr Ala | | | |
| 65 | 70 | 75 | 80 |
| Glu Leu Val Phe Met Ile Thr Asp Ala Leu Thr Ala Ile Ala Leu Tyr | | | |
| 85 | 90 | 95 | |
| Phe Ala Ile Gln Asp Phe Asn Lys Val Val Phe Lys Lys Gln Lys Leu | | | |
| 100 | 105 | 110 | |
| Leu Leu Glu Leu Glu Gln Tyr Ala Pro Asp Val Ala Glu Leu Ile Arg | | | |
| 115 | 120 | 125 | |
| Thr Pro Met Glu Met Arg Tyr Ile Pro Leu Lys Val Ala Leu Phe Tyr | | | |
| 130 | 135 | 140 | |
| Leu Leu Asn Pro Tyr Thr Ile Leu Ser Cys Val Ala Lys Ser Thr Cys | | | |
| 145 | 150 | 155 | 160 |
| Ala Ile Asn Asn Thr Leu Ile Ala Phe Phe Ile Leu Thr Thr Ile Lys | | | |
| 165 | 170 | 175 | |
| Val Ser Leu Ser Val Lys Trp Gly Gln | | | |
| 180 | 185 | | |

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

| | |
|---|-----|
| AAACCCTGTC GGTCTTGGAG CGACGACGGC AGAACCAGGG TCCCTGGCGG TGCGGCGGGG | 60 |
| CCGGCGGGTG CAGCGGAAGC GGCGGCGGCG GCGGCAGTGA CGTCGCCGGG AACCCTAAGG | 120 |
| ACTCTGCAAT ATGAATAATT CCCTAGAGAA CACCATCTCC TTTGAAGAGT ACATCCGAGT | 180 |
| AAAGGCACGG TCTGTCCCGC AACACAGGAT GAAGGAATTT CTGGACTCAC TGGCCTCTAA | 240 |

GGGGCCAGAA GCCCTTCAGG AGTTCCAGCA GACAGCCACC ACTACCATGG TGTACCAACA 300
GGGTGGGAAC TGCATATACA CAGACAGCAC TGAAGTGGCT GGGTCTTTGC TTGAACTTGC 360
CTGTCCAATC AC 372

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

CGGGAAGCTC GAAATGGAGA AGGTGAACCT TATGACCCAG ATGTGCTCTA CTATATTTTC 60
CTGTGTATTC AAAAGTATCT TTTTGAAAAT GGAAGGGTAG ATGACATTTT CTCCGATCTT 120
TATTATGTTT GGTTCACGGA GTGGCTACAT GAAGTTCTGA AGGATGTTCA GCCCCGGGTC 180
ACTCCACTTG GCTATGTCTT GCCCAGCCAC GTGACTGAGG AGATGCTATG GGAGTGCAAG 240
CAGCTTGGGG CTCACTCCCC CTCCACCTTG CTGACCACCC TCATGTTCTT TAATACCAAG 300
TAAGTGTTCT AGAGGCTCCA CTGCTGGCAT CTGTCCAGTG AAGAGTGTGG AACTATCCA 360
AGAGGCCTTC TGAATTCCTC TGACATATAT TTGAGAACT GGGCTACTGA AAGCCCTAAC 420
CCCACTTGGC TGCATTTTAT TTGGTAACCA GTGAGGCAAA CACCCTTGCC AGACCCTAC 480
CATCCATCTT GATGTGGTTC CTGCACTGGA CACTGCTTGG GTACGGGCCT GCCCAGATCT 540
TGGGAATGTG GGCAGTGGCT CCTCTGAAGC ACCAGTGGGC AGAGGATGAG TCATGGTATC 600
CT 602

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met Trp Phe Leu His Trp Thr Leu Leu Gly Tyr Gly Pro Ala Gln Ile
1 5 10 15

Leu Gly Met Trp Ala Val Ala Pro Leu Lys His Gln Trp Ala Glu Asp
20 25 30

Glu Ser Trp Tyr Pro
35

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 483 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

TGGGAAAGGG CTTGGACTGT GAAAAGAAAT GTGGCCCCTT TCCATCTTCA AGAGAGATGG 60
AATTAATGAT GGATGGACCC TGGAGGGAAT CTCCCCAGCC GACTTCCACT GGGCTGACAG 120
ACTTTGCTGA CCACAGGGGA ACGATGTTCT TTTCTTTCTT CATGATCAGA CATAAACTTA 180
GCATTTTAAT GGAAGAAAAA TGAGGGGAAC TTCAATTATG ATTTATTAAA GACAATTTCT 240
ATTACACCCT CCTTTATGAC AAGTGACATT TTAGATGTAA AAGTAAAAAC TTTACCATGC 300
CTTTTTTTTT TTTGTTGGCC TAACATTGAG GCCTTAAAAC CTGAGGCTCC TGTGCCTGAT 360
GGAATTCTTG TAACATACAC TTGTGTATCA TATAAGATA CCACTCTGTT TCTCTTATGT 420
ATTCTTACTC TAGTTGTTTA TTAAGAATGA CAAGCACGTC TTTTCAACAA AAAAAAAAAA 480
AAA 483

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1853 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CAGATTCGCT GCTGGAGTGC TGGATGGAGC CTTTCTCTGC CCTCTGTGAC ATTTCCAATT 60
 TTAGATAATG CCTCACATCT CTGTCCCCC GGGACCCCT GGAGCCCCCA TGATCCCTAA 120
 GAAGACAGCT TGAACCTAGA TCTACCCCC AGGATGTTGC GGAGGCTGCT GGAGCGGCCT 180
 TGCACGCTGG CCCTGCTTGT GGGCTCCCAG CTGGCTGTCA TGATGTACCT GTCACTGGGG 240
 GGCTTCCGAA GTCTCAGTGC CCTATTTGGC CGAGATCAGG GACCGACATT TGACTATTCT 300
 CACCCTCGTG ATGTCTACAG TAACCTCAGT CACCTGCCTG GGGCCCCAGG GGGTCTCCA 360
 GCTCCTCAAG GTCTGCCCTA CTGTCCAGAA CGATCTCCTC TCTTAGTGGG TCCTGTGTCTG 420
 GTGTCTTTTA GCCCAGTGCC ATCACTGGCA GAGATTGTGG AGCGGAATCC CCGGGTAGAA 480
 CCAGGGGGCC GGTACCGCCC TGCAGGTTGT GAGCCCCGCT CCCGAACAGC CATCATTTGTG 540
 CCTCATCGTG CCCGGGAGCA CCACCTGCGC CTGCTGCTCT ACCACCTGCA CCCCTTCTTG 600
 CAGCGCCAGC AGCTTGCTTA TGGCATCTAT GTCATCCACC AGGCTGGAAA TGGAACATTT 660
 AACAGGGCAA AACTGTTGAA CGTTGGGGTG CGAGAGGCCC TGCCTGATGA AGAGTGGGAC 720
 TGCCTGTTCT TGCACGATGT GGACCTCTTG CCAGAAAATG ACCACAATCT GTATGTGTGT 780
 GACCCCCGGG GACCCCGCCA TGTGCGGTT GCTATGAACA AGTTTGATA CAGCCTCCCG 840
 TACCCCCAGT ACTTCGGAAG AGTCTCAGCA CTTACTCCTG ACCAGTACCT GAAGATGAAT 900
 GGCTTCCCCA ATGAATACTG GGGCTGGGGT GGTGAGGATG ACGACTTGCT ACCAGGGTGC 960
 GCCTGGCTGG GATGAAGATC TCTCGGCCCC CCACATCTGT AGGACACTAT AAGATGGTGA 1020
 AGCACCGAGG AGATAAGGGC AATGAGGAAA ATCCCCACAG ATTTGACCTC CTGGTCCGTA 1080
 CCCAGAATTC CTGGACGCAA GATGGGATGA ACTCACTGAC ATACCAGTTG CTGGCTCGAG 1140
 AGCTGGGGCC TCTTTATACC AACATCACAG CAGACATTGG GACTGACCCT CGGGGTCTCTC 1200
 GGGCTCCTTC TGGGCCACGT TACCCACCTG GTTCTCTCCA AGCCTTCCGT CAAGAGATGC 1260
 TGCAACGCCG GCCCCAGCC AGGCCTGGGC CTCTATCTAC TGCCAACCAC ACAGCCCTCC 1320
 GAGGTTTACA CTGACTCCTC CTCCTGTCT ACCTTAATCA TGAAACCGAA TTCATGGGGT 1380
 TGTATTCTCC CCACCCTCAG CTCCTCACTG TTCTCAGAAG GATGTGAGGG AACTGAACTC 1440
 TGGTGCCGTG CTAGGGGGTA GGGGCCTCTC CCTCACTGCT GGACTGGAGC TGGGCTCCTG 1500
 TAGACCTGAG GGTCCNTCTY TCTAGGTCTC CTGTAGGGCT TAKGACTGTG AATCCTTGAT 1560
 GTCATGATTT TATGTGACGA TTCTTAGGAG TCCCTGCCCC TAGAGTAGGA GCAGGGYTGG 1620
 ACCCCAAGCC CNTCCYTYTT CCATGGAGAG AAGAGTGATC TGGYTTCTCC TCGGACCTCT 1680
 GTGAATATTT ATTCTATTTA TGGTTCCCGG GAAGTTGTTT GGTGAAGGAA GCCCCCTCCC 1740

TGGGCATTTT CTGCCTATGC TGGGAATAGCT CCCTCTTCTG GTCCTGGCTC AGGGGGCTGG 1800
 GATTTTGATA TATTTTCTAA TAAAGGACTT TGTCTCGCAA AAAAAAAAAA AAA 1853

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Arg | Arg | Leu | Leu | Glu | Arg | Pro | Cys | Thr | Leu | Ala | Leu | Leu | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gly | Ser | Gln | Leu | Ala | Val | Met | Met | Tyr | Leu | Ser | Leu | Gly | Gly | Phe | Arg |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ser | Leu | Ser | Ala | Leu | Phe | Gly | Arg | Asp | Gln | Gly | Pro | Thr | Phe | Asp | Tyr |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ser | His | Pro | Arg | Asp | Val | Tyr | Ser | Asn | Leu | Ser | His | Leu | Pro | Gly | Ala |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Pro | Gly | Gly | Pro | Pro | Ala | Pro | Gln | Gly | Leu | Pro | Tyr | Cys | Pro | Glu | Arg |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Ser | Pro | Leu | Leu | Val | Gly | Pro | Val | Ser | Val | Ser | Phe | Ser | Pro | Val | Pro |
| | | | 85 | | | | | 90 | | | | | | 95 | |
| Ser | Leu | Ala | Glu | Ile | Val | Glu | Arg | Asn | Pro | Arg | Val | Glu | Pro | Gly | Gly |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Arg | Tyr | Arg | Pro | Ala | Gly | Cys | Glu | Pro | Arg | Ser | Arg | Thr | Ala | Ile | Ile |
| | | | 115 | | | | 120 | | | | | 125 | | | |
| Val | Pro | His | Arg | Ala | Arg | Glu | His | His | Leu | Arg | Leu | Leu | Leu | Tyr | His |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Leu | His | Pro | Phe | Leu | Gln | Arg | Gln | Gln | Leu | Ala | Tyr | Gly | Ile | Tyr | Val |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Ile | His | Gln | Ala | Gly | Asn | Gly | Thr | Phe | Asn | Arg | Ala | Lys | Leu | Leu | Asn |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Val | Gly | Val | Arg | Glu | Ala | Leu | Arg | Asp | Glu | Glu | Trp | Asp | Cys | Leu | Phe |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Leu | His | Asp | Val | Asp | Leu | Leu | Pro | Glu | Asn | Asp | His | Asn | Leu | Tyr | Val |
| | | 195 | | | | | 200 | | | | | 205 | | | |

Cys Asp Pro Arg Gly Pro Arg His Val Ala Val Ala Met Asn Lys Phe
 210 215 220

Gly Tyr Ser Leu Pro Tyr Pro Gln Tyr Phe Gly Arg Val Ser Ala Leu
 225 230 235 240

Thr Pro Asp Gln Tyr Leu Lys Met Asn Gly Phe Pro Asn Glu Tyr Trp
 245 250 255

Gly Trp Gly Gly Glu Asp Asp Asp Leu Leu Pro Gly Cys Ala Trp Leu
 260 265 270

Gly

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1686 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

| | |
|--|-----|
| AGATAAAGTA AGTGCTGTTT GGGCTAACAG GATCTCCTCT TGCAGTCTGC AGCCCAGGAC | 60 |
| GCTGATTCCA GCAGCGCCTT ACCGCGCAGC CCGAAGATTC ACTATGGTGA AAATCGCCTT | 120 |
| CAATACCCCT ACCGCCGTGC AAAAGGAGGA GCGCGGCAA GACGTGGAGG CCCTCCTGAG | 180 |
| CCGCACGGTC AGAACTCAGA TACTGACCGG CAAGGAGCTC CGAGTTGCCA CCCAGGAAAA | 240 |
| AGAGGGCTCC TCTGGGAGAT GTATGCTTAC TCTCTTAGGC CTTTCATTCA TCTTGGCAGG | 300 |
| ACTTATTGTT GGTGGAGCCT GCATTTACAA GTACTTCATG CCCAAGAGCA CCATTTACCG | 360 |
| TGGAGAGATG TKCTTTTTTG ATTCTGAGGA TCCTGCAAAT TCCCTTCGTG GAGGAGAGCC | 420 |
| TAACTTCCTG CCTGTGACTG AGGAGGCTGA CATTCGTGAG GATGACAACA TTGCAATCAT | 480 |
| TGATGTGCCT GTCCCCAGTT TCTCTGATAG TGACCCTGCA GCAATTATTC ATGACTTTGA | 540 |
| AAAGGGAATG ACTGCTTACC TGGACTTGTT GCTGGGGAAC TGCTATCTGA TGCCCCCTCAA | 600 |
| TACTTCTATT GTTATGCCTC CAAAAATCT GGTAGAGYTC TTTGGCAAAC TGGCGAGTGG | 660 |
| CAGATATCTG CYTCAAACCT ATGTGGTTCG AGAAGACCTA GTTGCTGTGG AGGAAATTCG | 720 |
| TGATGTTAGT AACCTTGGA TCTTTATTTA CCAACTTTGC AATAACAGAA AGTCCTTCCG | 780 |
| CCTTCGTCGC AGAGACCTCT TGCTGGGTTT CAACAAACGT GCCATTGATA AATGCTGGAA | 840 |

GATTAGACAC TTCCCCAACG AATTTATTGT TGAGACCAAG ATCTGTCAAG AGTAAGAGGC 900
AACAGATAGA GTGTCCTTGG TAATAAGAAG TCAGAGATTT ACAATATGAC TTTAACATTA 960
AGGTTTATGG GATACTCAAG ATATTTACTC ATGCATTTAC TCTATTGCTT ATGCTTTAAA 1020
AAAAGGAAAA GAAAAAACT ACTAACCCT GCAAGCTCTT GTCAAATTTT AGTTTAATTG 1080
GCATTGCTTG TTTTTTGAAA CTGAAATTAC ATGAGTTTCA TTTTTTCTTT GAATTTATAG 1140
GGTTTAGATT TCTGAAAGCA GCATGAATAT ATCACCTAAC ATCCTGACAA TAAATTCCAT 1200
CCGTTGTTTT TTTTGTGTGT TTGTTTTTTC TTTTCCTTTA AGTAAGCTCT TTATTCATCT 1260
TATGGTGCAG CAATTTTAAA ATTTGAAATA TTTTAAATTG TTTTGAAC TTTTGTGTAA 1320
AATATATCAG ATCTCAACAT TGTGTTTTC TTTTGTTTTT CATTTTGTAC AACTTTCTTG 1380
AATTTAGAAA TTACATCTTT GCAGTTCTGT TAGGTGCTCT GTAATTAACC TGAATTATAT 1440
GTGAACAATT TTCATGAGAC AGTCATTTTT AACTAATGCA GTGATTCTTT CTCACTACTA 1500
TCTGTATTGT GGAATGCACA AAATTGTGTA GGTGCTGAAT GCTGTAAGGA GTTTAGGTTG 1560
TATGAATTCT ACAACCCTAT AATAAATTTT ACTCTATAAA AAAAAAAAAA AAAAAAAAAA 1620
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1680
AAAAAA 1686

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu Glu
1 5 10 15
Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg Thr Gln
20 25 30
Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu Lys Glu Gly
35 40 45
Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu Ser Phe Ile Leu
50 55 60

Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro
65 70 75 80

Lys Ser Thr Ile Tyr Arg Gly Glu Met Xaa Phe Phe Asp Ser Glu Asp
85 90 95

Pro Ala Asn Ser Leu Arg Gly Gly Glu Pro Asn Phe Leu Pro Val Thr
100 105 110

Glu Glu Ala Asp Ile Arg Glu Asp Asp Asn Ile Ala Ile Ile Asp Val
115 120 125

Pro Val Pro Ser Phe Ser Asp Ser Asp Pro Ala Ala Ile Ile His Asp
130 135 140

Phe Glu Lys Gly Met Thr Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys
145 150 155 160

Tyr Leu Met Pro Leu Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu
165 170 175

Val Glu Xaa Phe Gly Lys Leu Ala Ser Gly Arg Tyr Leu Xaa Gln Thr
180 185 190

Tyr Val Val Arg Glu Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val
195 200 205

Ser Asn Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser
210 215 220

Phe Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala
225 230 235 240

Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile Val
245 250 255

Glu Thr Lys Ile Cys Gln Glu
260

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

TNCACATTCTC AGTGGGAACT TGATGAAC

29

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

ANATATAGGTG GAATGAATTC TATCCTTG

29

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GNTATAGTAAT AATAGCACAA AGGACGGG

29

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TNGCCAGGAAA CCAAATCAAT GACTCTTT

29

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

TNTAATTGACG GTGTAGAGAA ATGAGGAA

29

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ANAAATGGAGC AGCTGGGTGG AGGCAAGA

29

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

TNCGGAGATAC TCCCAAGTCC AACAGTGA

29

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GNTTAGGGCTT TCACTAGCCC AGTTTCTC

29

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

ANTGACAGGTA CATCATGACA GCCAGCTG

29

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CNCGATGTTAG GTGATATATT CATGCTGC

29

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Glu | Val | Lys | Ser | Ser | Gly | Leu | Leu | Cys | Arg | Gly | Thr | Trp | Ala | Trp | 1 | 5 | 10 | 15 |
| Ser | Arg | Leu | Pro | Arg | Lys | Cys | Leu | Cys | Val | Gln | Ile | Ser | Arg | His | Leu | 20 | 25 | 30 | |
| Gly | Lys | Met | Tyr | Ser | Glu | Met | Ile | Phe | Val | Asn | Gly | Phe | Val | His | Cys | 35 | 40 | 45 | |
| Asp | Pro | His | Pro | Gly | Asn | Val | Leu | Val | Arg | Lys | His | Pro | Gly | Thr | Gly | 50 | 55 | 60 | |
| Lys | Ala | Glu | Ile | Val | Leu | Leu | Asp | His | Gly | Leu | Tyr | Gln | Met | Leu | Thr | 65 | 70 | 75 | 80 |
| Glu | Glu | Phe | Arg | Leu | Asn | Tyr | Cys | His | Leu | Trp | Gln | Ser | Leu | Ile | Trp | 85 | 90 | 95 | |
| Thr | Asp | Arg | Lys | Arg | Val | Lys | Glu | Tyr | Ser | Gln | Arg | Leu | Gly | Ala | Gly | 100 | 105 | 110 | |
| Asp | Leu | Tyr | Pro | Leu | Phe | Ala | Cys | Met | Leu | Thr | Ala | Arg | Ser | Trp | Asp | 115 | 120 | 125 | |
| Ser | Val | Asn | Arg | Gly | Ile | Ser | Gln | Ala | Pro | Val | Thr | Ala | Thr | Glu | Asp | 130 | 135 | 140 | |
| Leu | Glu | Ile | Arg | Asn | Asn | Ala | Ala | Asn | Tyr | Leu | Pro | Gln | Ile | Ser | His | 145 | 150 | 155 | 160 |
| Leu | Leu | Asn | His | Val | Pro | Arg | Gln | Met | Leu | Leu | Ile | Leu | Lys | Thr | Asn | 165 | 170 | 175 | |
| Asp | Leu | Leu | Arg | Gly | Ile | Glu | Ala | Ala | Leu | Gly | Thr | Arg | Ala | Ser | Ala | 180 | 185 | 190 | |
| Ser | Ser | Phe | Leu | Asn | Met | Ser | Arg | Cys | Cys | Ile | Arg | Ala | Leu | Ala | Glu | 195 | 200 | 205 | |
| His | Lys | Lys | Lys | Asn | Thr | Cys | Ser | Phe | Phe | Arg | Arg | Thr | Gln | Ile | Ser | 210 | 215 | 220 | |
| Phe | Ser | Glu | Ala | Phe | Asn | Leu | Trp | Gln | Ile | Asn | Leu | His | Glu | Leu | Ile | 225 | 230 | 235 | 240 |
| Leu | Arg | Val | Lys | Gly | Leu | Lys | Leu | Ala | Asp | Arg | Val | Leu | Ala | Leu | Ile | 245 | 250 | 255 | |
| Cys | Trp | Leu | Phe | Pro | Ala | Pro | Leu | 260 | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

| | |
|--|------|
| CGCTTTTTTT TTTTTTTTTT TTCAGAAGGA GGAAGCTCAT TATGTTTGA TCACCCACAG | 60 |
| CTATAGATTC TAAAAATATT TTGGCTTTTT TTGAGGTGCT TTAGTAAAAT ATAACCCCAA | 120 |
| ATGATTCACT TGGACAAGTG GTCTTAACAG CAAGGAAAAC AAACACTTTA TGAAAACAGC | 180 |
| TATAAGCCTT CTGTCTTTTA TCTTTACTAT TTTCTCCGAG TCTGGCATGA AACAGATACA | 240 |
| CAGCAGCCTC CACAGGGGGT TAAGTARAGA ACCATCCAAG CATCACAGAG TGTCATCCAG | 300 |
| AATTCTGATG ACTTCCATTC GTTGA CTCTG ATGCACAATA TGCCTGGCTT GGGATGCAGC | 360 |
| GACCATGATG CCCCTCCCAG AACAGACACT TGCAGAGTGT TCCAGGAACA GCAGCTCCCT | 420 |
| CCAGCCCCCA GCACAAGATG CACACATCTC AGAACAAGCC TCCATCCTTT TCCTAGAGAA | 480 |
| CTGAGCATAA ATAACCTGTT CTATATCTGG CTCCAAGTCC ATTTCTGTTC TGTCTTGGAG | 540 |
| TAGAGTCTTA GCTCCCAGTT TGTTTTAGGT CAACTTTCAG CACCTACTTC AGCTCACTTG | 600 |
| TTTGATTTAC TAAGCTCTTG CTTCTGTATA TTATCAAATG TAGGGATGTA GGGAGAATAA | 660 |
| AAGGATCTAG AACTTGGCTT TTAGGAGAGA TTAGAACAAA GCTGAAGGTG GAGGCATTAG | 720 |
| TTCTAGGTC TTCAGATCTC AGAGCAAAGG ACCCACTCTG GAGCCTAAAT TCTATGAGAG | 780 |
| ACCACAGAGC AGCCTGAAAT CCAAAGGAGT TTTACACAGG AAAAAAAAAA TACTGTGAGG | 840 |
| ACTTACACTA AATAATAATG TTGTTTGA TGGGGTTGTG GGTAATTCCT ATATTCTTCT | 900 |
| TTATAACTTT TGTACTTTTC AAATCCCTA ATGTGAACTC ACTACTTAGT AGGTCTGTAA | 960 |
| GCTTAAACAT TACTATGGCT TGGAATCTCA TTTCAAAAAA TCTTTAAAAT GGGGACAAGA | 1020 |
| GTAAAAATTT CTTAGCTTCT ATGGAAGAAT AAAATGAAAT TATAATGATA CAGTGCCTGG | 1080 |
| CATGTTGTGG TCGCTCAATA AACACTGCTT TCCTCCCCAT TGTCTCTCTC TTTATTCTGT | 1140 |
| TTCATTACAA GGTGAGCAGA TTGAATCAGG ACCAGCTGGG AGGGCTACTT CTATGAGAGA | 1200 |
| AGATCTGTCC ACAGTCATGG TTTTCAATGT TTAGTGCACC AGAATCACCT TGAGGGTTTG | 1260 |
| TTAAAACAGA CTGCTGAACA TAACACATCT ATGAGAATGG CCAAAATCCA GAACACCAAA | 1320 |
| TGCTGGTGAG GATGTGGAGC AATAAAAACT CTCATTTATT GCTGATGGCA ATGCAAAATG | 1380 |

GTACAGCCAC TTTGGAAGAC AATTTGCCAA ATTTTACAA AACTAAGTGT ACTCTTACCA 1440
TACAATCTAG CAATCATGCT CCCTGGTATT TACCTAAAGG AGTTAAAAAC TTATGTCTAG 1500
ACAGAAACCT GCATATGAAT GTTTATAGCA GTTTTTTTCA TAATTGCTAA ACTTTGGAAG 1560
TAACCAAGAT GCCCTTCAGC AGGTGAATGG ACAAATAAAC TGCAGTAGAT GCAGACAGTG 1620
GAATATCATT CTAGGCCATG AAGGCCGAAT TCGGCCTTCA TGGCCTAATT AAAGAAAGTC 1680
AGGATAAAAA TTTTAAAAAG CAGGCCACTG TCAGCAAAGC CTGGAGAAGT GGGGCCGGAG 1740
GYTCCGCCCC CATCATGTGC CTGCCACCCC TTCCCAGTCA TCCCTTTAYT CTTACAGTAG 1800
CAAATAAGAC CCCTGTCTAA TGGGGGGAGA CAAATGTGTA GACCCTTAGC CACCTTGGCC 1860
AGGGCTGACT CCTTAAATTT CTGGATGATG ATGATTGTTA TTTAATAGCC AGAGGCTCAT 1920
ATAATTGGCC TCTTTGGAAG AGGCCTCATG GCCTCCTTAC TCTCACCAA GCAATTTTTC 1980
CCTCAGGGGG GCTCCCATCT TCTTACACAG AGAGGCAGCT GAGGCAGGAC AGTGGGGCTA 2040
ACTGTAGACC AGGCGAGGGC ACGGGCTGCT GGGGTGGCCC TGCTTCCCCA GTGTACATAT 2100
TGTATCTGTG TAACATTTTG TATATTCCAG GGGTAGGGCC GCCCCCTGTA TCATACCTAG 2160
CAGAGGTTGG AGCTGGCACA TGGGGAGGAG GTTCTAATAA TTATTGGGG CTGGGAAACT 2220
TATTTATTGA TAGCATAGGA CAGAGGAAGG AGGCGGGGAT GGGGTCGTGG CGCCCTGGTG 2280
ATGCGACTCC TGTTTATTTT GCTTTTATT TCGGAATAAA TGGATTTAGC CATAAAAAAA 2340
AAAAAAAAAA AAAAA 2355

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Thr | Ala | Ile | Ser | Leu | Leu | Ser | Phe | Ile | Phe | Thr | Ile | Phe | Ser |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Glu | Ser | Gly | Met | Lys | Gln | Ile | His | Ser | Ser | Leu | His | Arg | Gly | Leu | Ser |
| | | | 20 | | | | 25 | | | | | 30 | | | |
| Xaa | Glu | Pro | Ser | Lys | His | His | Arg | Val | Ser | Ser | Arg | Ile | Leu | Met | Thr |
| | | | 35 | | | | 40 | | | | | 45 | | | |

Ser Ile Arg
50

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

| | |
|---|------|
| GCGCCCTTTC GGTCAACATC GTAGTCCACC CCCTCCCCAT CCCAGCCCC CGGGGATTCA | 60 |
| GGCTCGCCAG CGCCAGCCA GGGAGCCGGC CGGGAAGCGC GATGGGGGCC CCAGCCGCCT | 120 |
| CGCTCCTGCT CCTGCTCCTG CTGTTGCGCT GCTGCTGGGC GCCCGGCGGG GCCAACCTCT | 180 |
| CCCAGGACGA CAGCCAGCCC TGGACATCTG ATGAAACAGT GGTGGCTGGT GGCACCGTGG | 240 |
| TGCTCAAGTG CCAAGTGAAA GATCACGAGG ACTCATCCCT GCAATGGTCT AACCTGCTC | 300 |
| AGCAGACTCT CTACTTTGGG GAGAAGAGAG CCCTTCGAGA TAATCGAATT CAGCTGGTTA | 360 |
| CCTCTACGCC CCACGAGCTC AGCATCAGCA TCAGCAATGT GGCCCTGGCA GACGAGGGCG | 420 |
| AGTACACCTG CTCAATCTTC ACTATGCCTG TGCGAACTGC CAAGTCCCTC GTCACTGTGC | 480 |
| TAGGAATTCC ACAGAAGCCC ATCATCACTG GTTATAAATC TTCATTACGG GAAAAAGACA | 540 |
| CAGCCACCCT AAAGTGTCTG TCTTCTGGGA GCAAGCCTGC AGCCCGGCTC ACCTGGAGAA | 600 |
| AGGGTGACCA AGAACTCCAC GGAGAACCAA CCCGCATACA GGAAGATCCC AATGGTAAAA | 660 |
| CCTTCACTGT CAGCAGCTCG GTGACATTCC AGGTTACCCG GGAGGATGAT GGGGCGAGCA | 720 |
| TCGTGTGCTC TGTGAACCAT GAATCTCTAA AGGGAGCTGA CAGATCCACC TCTCAACGCA | 780 |
| TTGAAGTTTT ATACACACCA ACTGCGATGA TTAGGCCAGA CCCTCCCCAT CCTCGTGAGG | 840 |
| GCCAGAAGCT GTTGCTACAC TGTGAGGGTC GCGGCAATCC AGTCCCCCAG CAGTACCTAT | 900 |
| GGGAGAAGGA GGGCAGTGTG CCACCCCTGA AGATGACCCA GGAGAGTGCC CTGATCTTCC | 960 |
| CTTTCCTCAA CAAGAGTGAC AGTGGCACCT ACGGCTGCAC AGCCACCAGC AACATGGGCA | 1020 |
| GCTACAAGGC CTACTACACC CTCAATGTTA ATGACCCAG TCCGGTGCCC TCCTCCTCCA | 1080 |
| GCACCTACCA CGCCATCATC GGTGGGATCG TGGCTTTCAT TGTCTTCCTG CTGCTCATCA | 1140 |
| TGCTCATCTT CCTCGGCCAC TACTTGATCC GGCACAAAGG AACCTACCTG ACACATGAGG | 1200 |
| CAAAAGGCTC CGACGATGCT CCAGACGCGG ACACGGCCAT CATCAATGCA GAAGGCGGGC | 1260 |

| | |
|--|------|
| AGTCAGGAGG GGACGACAAG AAGGAATATT TCATCTAGAG GCGCCTGCCC ACTTCCTGCG | 1320 |
| CCCCCAGGG GCCCTGTGGG GACTGCTGGG GCCGTCACCA ACCCGGACTT GTACAGAGCA | 1380 |
| ACCGCAGGGC CGCCCCTCCC GCTTGCTCCC CAGCCCACCC ACCCCCCTGT ACAGAATGTC | 1440 |
| TGCTTTGGGT GCGGTTTTGT ACTCGGTTTG GAATGGGGAG GGAGGAGGGC GGGGGGAGGG | 1500 |
| GAGGGTTGCC CTCAGCCCTT TCCGTGGCTT CTCTGCATTT GGGTTATTAT TATTTTTGTA | 1560 |
| ACAATCCCAA ATCAAATCTG TCTCCAGGCT GGAGAGGCAG GAGCCCTGGG GTGAGAAAAG | 1620 |
| CAAAAAACAA ACAAAAAACA AAACCCTGGA GTGTTAGGAG GAGAGTGAAG GTAGAGGGGT | 1680 |
| GAGGAAGGGT AAGGGGCAGG GCTGGTTTCA GCTGGGGGCT CTCACCAGCC CTCCTTTCAG | 1740 |
| CCTCTACAAC AGAGCAGCTT CCCAGACTTC TCCAGGAACC CAGAAACGGG ATGGTTGTCTG | 1800 |
| GCAAAGGTTG GGAGTGGCTT TTCCTCTGGT AGCCACACAC CTGAGCACTA CGGACAGGGA | 1860 |
| GGCAGGTGCC ACCTTGACAC CTCTCTTCCA TAGCAATGGG AAAGTGATGA GTGCGGGAGT | 1920 |
| CCTGAGGAGA TGTGGCCTGC AGACAACATG CAGCCATGCA GGGACCCAGG ACTGTAACCT | 1980 |
| GGGGAGGACG CGGGTCCCTG CAAGGAAGAG TAGATTTGGA GAGGAAGGAT GGAGGTGGAC | 2040 |
| TCTCACCCCA TTCCCCCGG AAATGAACAA AGCCGGGCCC TTTCCATAGG AACTGCCCTT | 2100 |
| GGAGATAGCA GAGTGTGGCT GCCCCTCCTT GCTCCAGCAG CAGTGGGAGA GGCAGTCTC | 2160 |
| TGGGGCCTGA ACTGCCTCTG CTTCCCCCCC TGAGGGGCCC CTCACTCTTA CCAAGACTC | 2220 |
| TGGATTGTTG CACGGCAACC ACTCCTCCCA TGGCATTGCT CAGCAACTAC TTCTCCCTTC | 2280 |
| CCGGCCACCC TGTGCCCCCT TCCTGGTCCC AACGCCAGCC CTTTCATCCTT CCTCCCTCAG | 2340 |
| CAGCCAGGCA GACATAACAA CAAAACACT AAAAGGAGCT TCAAAAAAA AAAAAAAAAA | 2400 |
| AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA | 2460 |
| AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA | 2496 |

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 398 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Phe Ala

| | | | |
|-------------|-------------------------|---------------------|-----------------|
| 1 | 5 | 10 | 15 |
| Cys Cys Trp | Ala Pro Gly Gly Ala | Asn Leu Ser Gln | Asp Asp Ser Gln |
| | 20 | 25 | 30 |
| Pro Trp Thr | Ser Asp Glu Thr Val | Val Ala Gly Gly Thr | Val Val Leu |
| | 35 | 40 | 45 |
| Lys Cys Gln | Val Lys Asp His Glu | Asp Ser Ser Leu | Gln Trp Ser Asn |
| | 50 | 55 | 60 |
| Pro Ala Gln | Gln Thr Leu Tyr Phe Gly | Glu Lys Arg Ala | Leu Arg Asp |
| 65 | 70 | 75 | 80 |
| Asn Arg Ile | Gln Leu Val Thr Ser Thr | Pro His Glu Leu | Ser Ile Ser |
| | 85 | 90 | 95 |
| Ile Ser Asn | Val Ala Leu Ala Asp | Glu Gly Glu Tyr Thr | Cys Ser Ile |
| | 100 | 105 | 110 |
| Phe Thr Met | Pro Val Arg Thr Ala | Lys Ser Leu Val Thr | Val Leu Gly |
| | 115 | 120 | 125 |
| Ile Pro Gln | Lys Pro Ile Ile Thr | Gly Tyr Lys Ser Ser | Leu Arg Glu |
| | 130 | 135 | 140 |
| Lys Asp Thr | Ala Thr Leu Asn Cys Gln | Ser Ser Gly Ser Lys | Pro Ala |
| 145 | 150 | 155 | 160 |
| Ala Arg Leu | Thr Trp Arg Lys Gly Asp | Gln Glu Leu His Gly | Glu Pro |
| | 165 | 170 | 175 |
| Thr Arg Ile | Gln Glu Asp Pro Asn Gly | Lys Thr Phe Thr Val | Ser Ser |
| | 180 | 185 | 190 |
| Ser Val Thr | Phe Gln Val Thr Arg | Glu Asp Asp Gly Ala | Ser Ile Val |
| | 195 | 200 | 205 |
| Cys Ser Val | Asn His Glu Ser Leu Lys | Gly Ala Asp Arg Ser | Thr Ser |
| | 210 | 215 | 220 |
| Gln Arg Ile | Glu Val Leu Tyr Thr Pro | Thr Ala Met Ile Arg | Pro Asp |
| 225 | 230 | 235 | 240 |
| Pro Pro His | Pro Arg Glu Gly Gln Lys | Leu Leu Leu His Cys | Glu Gly |
| | 245 | 250 | 255 |
| Arg Gly Asn | Pro Val Pro Gln Gln Tyr | Leu Trp Glu Lys Glu | Gly Ser |
| | 260 | 265 | 270 |
| Val Pro Pro | Leu Lys Met Thr Gln Glu | Ser Ala Leu Ile Phe | Pro Phe |
| | 275 | 280 | 285 |
| Leu Asn Lys | Ser Asp Ser Gly Thr Tyr | Gly Cys Thr Ala Thr | Ser Asn |
| | 290 | 295 | 300 |
| Met Gly Ser | Tyr Lys Ala Tyr Tyr Thr | Leu Asn Val Asn Asp | Pro Ser |

| | | | | | | |
|---|--|-----|--|-----|--|-----|
| 305 | | 310 | | 315 | | 320 |
| Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile | | | | | | |
| | | 325 | | 330 | | 335 |
| Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly | | | | | | |
| | | 340 | | 345 | | 350 |
| His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys | | | | | | |
| | | 355 | | 360 | | 365 |
| Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu | | | | | | |
| | | 370 | | 375 | | 380 |
| Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile | | | | | | |
| | | 385 | | 390 | | 395 |

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2764 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

| | |
|--|-----|
| GGGCCAAAGA GGCCTACCAG CTGCTGTTGA CCGCTGGACT CACAAACCTT TCTTTCTACT | 60 |
| CTTGTTTTTC ATTCACTTTG GGTCATTTTT CAGTGTTGAT GGGGACGTAA TAAAGCACGG | 120 |
| TAAGAAAATC CGTGAATTCC GTCAGAGCAG TCGTCCAGAG GGAAGGCGCG CCCGGCGTAG | 180 |
| GGAGGTCAGA GCTCATGTTA GCTATGAACA CAGGTCACAG GGGCGTACGG CGATGGGAAA | 240 |
| CACTGAGATG CTCAATATAT TGATTATTTA ATAGTGTTTA GCAAAATGGT CTTTTTTTAT | 300 |
| TCCTTAAATC AACTGAAACT CACTTCACGT CTCTTCCTT GTAGAGCATC ATGCTTATTT | 360 |
| CTGGCTCACT CACATCTTTG TCTCGGGAGT TCTCTGCCGA GCCATTGCCC CCTACAGCAG | 420 |
| AGAGCACAGC TGGCTGCACT AGTGCTGAAG GAGCCAGCCC CAGAGCAGGG CATTTCCAGG | 480 |
| GGCTCTTGTC CCAGAGCGGC AGGCGTTGTG TGCAGAGAAC GCCCCTCCCA CGCAGCACAG | 540 |
| AGAACGCGGG GTGGGTGTGT GGCTCCGGGC CTGTGGGGCT TAGGCTGCCT GAACCACCGC | 600 |
| CGACTGGCAC CATGACTCGG CATTCCTGGA AGTGCCTTAC CAAGTTGTTG TTGTTGTTTT | 660 |
| GTGTTTTTTT AAGAGACGGG CTTGCTCTAT CATCCAGGCT CGAGTGCAAT GGCACAGTCA | 720 |
| CAGCTCACTG CAGCCTTGAA CTCGTGGGGCT CAAGCCATCC TCCTGTGTCA GCCTCCCCAG | 780 |

| | | | | | | |
|------------|------------|-------------|------------|------------|-------------|------|
| TACCTGGGAC | TGTGGGCATG | AGCACTGCGC | CTGGCAGCTG | TATCAGTGTT | GACTCCACAT | 840 |
| TTTAATAGTT | GCTTCTTGAA | ATTAAAAATGC | TTTGATTGAG | CCTTCAAGCC | ATCAGGAAAG | 900 |
| TTTGCCCTC | TGAGTCACAC | CTGGTGGTCT | CCAGGGTTCC | TGCCCCCTCC | TCCTGAGCCA | 960 |
| GCTCCTCAGA | GCGGATAGAG | GCAGGACCCC | CACCCAGGTC | TTGAGACCCC | CCTGCCCCGC | 1020 |
| ACTCCCCCGG | AGACGGGCTA | CCCCTGCAGA | TGCAGATAGT | CAAAGCTCAG | GTTTCTTCCA | 1080 |
| AAGCTTTTAA | AAAGATATTG | TACCTTGAGC | ACTTTAAAAA | TGTCTTAAAA | TTGCCATACA | 1140 |
| GGCTCTTAAA | AGCTTATACG | TTTAAACTGT | TGATAGATGG | GCCTTTACTA | AAATGCATTC | 1200 |
| ATTTATTTTC | CTAATCCCTT | GGTTGTTAAA | TAATTCTGGG | GAAGGGCCCC | GAGCACGACA | 1260 |
| GCCGCAGTCT | CCACCCAGAA | CCAGAGAGTC | CCCCCAACC | CGGGATGTAC | CCTCTGGCCA | 1320 |
| CACCAGGGAC | CCTGCCAGAG | GCCGCAGACT | GGCAGCAGCA | GCCTCCCCAC | ACAGTGGGGG | 1380 |
| AAGGTCAGTG | TGATGCCTTC | AGGCCCCGTC | TCCTGCCAGG | GCTCTCCCTC | CAGCCTACAT | 1440 |
| AGGGCCTCAG | AGAAATGCAT | TTTTAGTTCT | GGCTTTGGCC | CAGCCCAGGG | CAAGGCAGGA | 1500 |
| AACTCTCCAG | CGTGAGTCCG | TGAGGGCCAA | GAAGTCCCGC | CCTGTTCTGG | GGGAGGACCT | 1560 |
| GGCTTTTCTG | GTGTCTCTGG | TGCCCCGAGAG | CCCGGTGCTG | CCATCTTTAG | TGAAAGAGTA | 1620 |
| AATGGTGGCC | GAGGGCTCCT | TTTGTGAGGG | ATGTGCCTTG | GTGAAGAAGG | CATGTTCCCT | 1680 |
| GCCGTGAAGA | TACTTGGAAG | CTCTGGGTGG | AGAGGGAAAA | GGGATACCCC | TGGTGCTCCC | 1740 |
| TGGGCCTGGC | GGAAGGCTAG | GAGGAAGGAC | AGCTGAGGTG | AGGACTGAGT | GGGGCAGGTA | 1800 |
| TCACCCTGAC | AAACAGTTTG | GGAAGATCAG | GAAAGGCAGG | TGAGACCTGG | TGCAGAATCC | 1860 |
| AGGTTGGGTA | ATAGATACAT | CGTCGAAGAT | GTAGCAAGCA | AAGTAATATA | CTCAACTCTG | 1920 |
| GAACATTGCA | CAGAAGCTTT | TAAAGCACTC | TGTGACACTT | TTTGTAATGA | GGGATCTGAA | 1980 |
| GGAAACGGCC | CCAGAGTCAC | CCATCCCCAC | GGGTCTGGTT | GGCGGGGCTG | GTGCCTTTCT | 2040 |
| TCTGCACTCA | GTCACCATGG | CTCCGTCTGT | CAAACCAAC | TCTTTTTTTT | TTTTTTTTTTC | 2100 |
| TTCTCTTGGT | GTGGTAATTT | GTTTGAAGAG | CCACTCCATC | CCCAAATTCA | AGATTAGAAA | 2160 |
| GATCCCTGAC | TGCTTCTCAA | GATCCAGAAC | ATTCCTTGAC | AGAGTATATT | CACCATTTAG | 2220 |
| AAGTGATCCA | GCAAAGATTG | GGAGGGGTAC | TACCAGATTC | TACTTCAAAG | AAATCCTGCC | 2280 |
| ACCCGATGAT | TAAACAGTGA | ATAAAATGTC | ATGGCTCTTT | CCTGCGACAA | TTCTATTTGA | 2340 |
| GGAAAAGATT | TGTTTTTCCC | TTTTCCCAAG | GAAGCTCGTG | GGACAGCATG | GGCACTACTC | 2400 |
| TTCATGTGCG | GTGACACCAG | CCCCCAGATG | CCTTGAATTA | AGTGTCTCTA | CCTTTATGCA | 2460 |
| TGACTGCAAA | GCCAGCTGGA | GCATTTTCTA | TGGAGCCTCC | GTATGTTTTA | GGCCCATGAC | 2520 |

CTTCGTGAGG TGATGGGCAC TCACTCCCAT GAGCCCTGGC TGTGTGCTGT TGTGTGCCTA 2580
 TCGGCAGATC CATCCTTCCT GCCTCCAAGG AGGATACACA GAGAATGGCT TCCTGTTGTT 2640
 TTGTTTATTT TCTTAACGTG TACAGATGGA AACTTCATTT AAAAATAAAA ACAAACAAY 2700
 TCNAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2760
 AAAA 2764

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ile | Ser | Gly | Ser | Leu | Thr | Ser | Leu | Ser | Arg | Glu | Phe | Ser | Ala | 1 | 5 | 10 | 15 |
| Glu | Pro | Leu | Pro | Pro | Thr | Ala | Glu | Ser | Thr | Ala | Gly | Cys | Thr | Ser | Ala | 20 | 25 | 30 | |
| Glu | Gly | Ala | Ser | Pro | Arg | Ala | Gly | His | Phe | Gln | Gly | Leu | Leu | Ser | Gln | 35 | 40 | 45 | |
| Ser | Gly | Arg | Arg | Cys | Val | Gln | Arg | Thr | Pro | Leu | Pro | Arg | Ser | Thr | Glu | 50 | 55 | 60 | |
| Asn | Ala | Gly | Trp | Val | Cys | Gly | Ser | Gly | Pro | Val | Gly | Leu | Arg | Leu | Pro | 65 | 70 | 75 | 80 |
| Glu | Pro | Pro | Pro | Thr | Gly | Thr | Met | Thr | Arg | His | Ser | Trp | Lys | Cys | Leu | 85 | 90 | 95 | |
| Thr | Lys | Leu | Leu | Leu | Leu | Phe | Cys | Cys | Phe | Leu | Arg | Asp | Gly | Leu | Ala | 100 | 105 | 110 | |
| Leu | Ser | Ser | Arg | Leu | Glu | Cys | Asn | Gly | Thr | Val | Thr | Ala | His | Cys | Ser | 115 | 120 | 125 | |
| Leu | Glu | Leu | Val | Gly | Ser | Ser | His | Pro | Pro | Val | Ser | Ala | Ser | Pro | Val | 130 | 135 | 140 | |
| Pro | Gly | Thr | Val | Gly | Met | Ser | Thr | Ala | Pro | Gly | Ser | Cys | Ile | Ser | Val | 145 | 150 | 155 | 160 |
| Asp | Ser | Thr | Phe | | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

| | |
|---|------|
| CAGAAGGGAG GTAGTCGCCC TCCGTCGTGG CCTGGCGTGG ATTCCGAGCG TTGGTGTCTG | 60 |
| GCGGTTTCCG ACCGTTGGTG TCTGGCACGC GCCACCCCGA TGTACCAGGT AAAGCCCTAT | 120 |
| CACGGGGTCG GCGCCCCTCT CCGTGTGGAG CCCACCTGCA TGTACTGGCT CCCCAACATG | 180 |
| CACGGCAGGA GCGGCGGCCC AGCACTCGGC ACTGGCCACT TGCAGACAAG AAGACAAGAA | 240 |
| AATGATTTGA GGACAGCTTC AATCGCGGTG TGAAGAAGAA AGCAACAAAA CGACCACTGA | 300 |
| AAACAATGCC GGTGGCAAAA CATCCAAAGA AAGGGTCCCA AGCGGTACAT CGTCATAGCT | 360 |
| GGAAACAGTC AGAGCCACCA GCCAATGATC TTTTCAATGC TGCGAAAGCT GCCAAAAGTG | 420 |
| ACATGCAGTG TGGCCATGAG GTCTGCCGGA AGTGA CTGTGTATC TCCTGAGTTA | 480 |
| AAATGTGAAG GGATTTTTTT TTTTCAGATT ACTGAGAGTC TTCTGT TACT AGTTTGTCTT | 540 |
| TCCTAGATCC AGACACGGGG ACTGCAGAGA AAGGCTGTGT GCATCCGCTG TCTACTCCAC | 600 |
| TGTCTCCTCT GCAGAGGCGG ATTTCCCTGA CTGAAGACCA TGTTCAGGC CCACAGCTGC | 660 |
| CTACAGAACC GTCCCAAAAT ATGGCAAAGA AACCTATTCT GAGGGTCTCA CCATGTTGCC | 720 |
| CAGGCTGGTC TTGAACTCCT GGA CT CATCC TAAAGTGCTG GCCTCTCATT CCCTGTCTGT | 780 |
| GCACACCTCA CGGCAAGGGC CAGCCTGTTT CCTCCCGGTC ACCTCCAAAT CTTGCTGCTT | 840 |
| TTAATTCAAC TCAGAGGCCT AGCCAGGGTT GAGTTCTCAC CCACCTGTGC CGCCCTGCCT | 900 |
| TGTTACCTGG AAGCACAGCC TTGGGGACTG AGCAGGCCCT CACTGTCACT TTAAGAAGGG | 960 |
| AATCAGCCAC TTTGTGCTCA CCACCTCTGG GGAAGGTGTG AGAGGAGAGA AGGAAGTGGC | 1020 |
| TGTTTGGCTG CTGACAACAT GAAGACTTCC TGCATGAGA ACAGAGGCAC AGGTGCCGGC | 1080 |
| CCTGCAGCCC CCAGAACCCG GACTGGAGGG GGCCATGGGG CGCCGGACCC TGGCCCTGCC | 1140 |
| CTGGGTGCTG CTGACCCTGC GTGTCACTGC AGGGACCCCG GAGGTGTGAG TACAAGTTCTG | 1200 |
| GATGGAGGCC ACCGAGCTCT CGTCCTTCAC CATCCGTTGT GGGTTCCTGG AGTCTGGCTC | 1260 |
| CATCTCCCTG GTGACTGTGA GCTGGGGGGG CCCCATGGT GCTGGGGGGA CCACGCTGGC | 1320 |

| | | | | | | |
|-------------|------------|------------|-------------|------------|-------------|------|
| TGTGTTGCAC | CCGGAACCTG | GCATCCAGCA | ATGGGCCCCCT | GCTCGCCAGG | CCCGCTGGGA | 1380 |
| AACCCAGAGC | AGCGTCTCTC | TTGCCCTGGA | AGTCTCTGGG | GCCAGCAGCC | CCTGCACCAA | 1440 |
| CACCACCTTC | TGCTGCAAGT | TTGCGTCCTT | CCCTGAGGGC | TCCTGGGAGG | CCTCTGGGAG | 1500 |
| CCTCCCGCCC | AGCTCAGACC | CAGGGCTCTC | TGTCCCGCCG | ACTCCTGCCC | CCATTCTGCG | 1560 |
| GGCAGACCTG | GCCGGGATCT | TGGGGGTCTC | AGGAGTCCTT | CTCTTTGACT | GTGGCTACCT | 1620 |
| CCTTCATCTG | CTGTGCCGAC | AGAAGCACCG | CCCTGCCCCCT | AGGCTCCAGC | CATCCCACAC | 1680 |
| CAGCTCCTAG | GCACTGAGAG | CACGAGCATG | GGCACCCAGC | CAGGCCTCCC | AGGCTGCTCT | 1740 |
| CCACGTCCCT | TATGCCACTA | TCAACACCAG | CTGCTGCCCA | GCTACTTTGG | ACACAGCTCA | 1800 |
| CCCCCGACAG | GGGGCCGTCC | TGTCGTTTCC | TGCTGTGACT | AAGTCAGCAA | CACAGTTCCT | 1860 |
| CTGACATGGG | CCTTGGCTGT | GCTTCTTTGG | GGGTGAAGAG | ATTGGGGAGG | AAGTCTCCAC | 1920 |
| CCCTGGGAGG | CAGAAGCCAG | GCATAGCGCG | CTGGCTAGGA | CTCCAGTACC | GTGAAGGGAG | 1980 |
| GCAGTGAGAG | CAGACATCTG | TGTCTCATTC | CTGATCTCAA | GGGGAAAGCA | AGAACAAGGG | 2040 |
| AGGCTTCCTC | AGGATCTCAA | ACCTGCGGAA | GGAGGACCAG | TCTGTGTACT | TCTGCCAAGT | 2100 |
| CCAGCTGGAC | ATACAGATCA | GCCCTCAGGC | AGCCCCTCCA | CAGGACCCCT | CTCCTGCCTG | 2160 |
| GACAGCTCTG | CTGGTCTCCC | CGTCCCCTGG | AGAAGAACAA | GGCCATGGGT | CGGCCCCCTGC | 2220 |
| TGCTGCCCCCT | GCTGCTCCTG | CTGCAGCCGC | CAGCATTTCT | GCAGCCTGGT | GGCTCCACAG | 2280 |
| GATCTGGTCC | AAGCTACCTT | TATGGGGTCA | CTCAACCAAA | ACACCTCTCA | GCCTCCATGG | 2340 |
| GTGGCTCTGT | GGAAATCCCC | TTCTCCTTCT | ATTACCCCTG | GGAGTTAGCC | ACAGCTCCCG | 2400 |
| ACGTGAGAAT | ATCCTGGAGA | CGGGGCCACT | TCCACGGGCA | GTCCTTCTAC | AGCACAAGGC | 2460 |
| CGCCTTCCAT | TCACAAGGAT | TATGTGAACC | GGCTCTTTCT | GAAGTGGACA | GAGGGTCAGG | 2520 |
| AGAGCGGCTT | CCTCAGGATC | TCAAACCTGC | GGAAGGAGGA | CCAGTCTGTG | TATTTCTGCC | 2580 |
| GAGTCGAGCT | GGACACCCGG | AGATCAGGGA | GGCAGCAGTT | GCAGTCCATC | AAGGGGACCA | 2640 |
| AACTCACCAT | CACCCAGGCT | GTCACAACCA | CCACCACCTG | GACGCCCAGC | AGCACAACCA | 2700 |
| CCATAGCCGG | CCTCAGGGTC | ACAGAAAGCA | AAGGGCACTC | AGAATCATGG | CACCTAAGTC | 2760 |
| TGGACACTGC | CATCAGGGTT | GCATTGGCTG | TCGCTGTGCT | CAAAACTGTC | ATTTTGGGAC | 2820 |
| TGCTGTGCCT | CCTCCTGTGG | TGGAGGAGAA | GGAAAGGTAG | CAGGGCGCCA | AGCAGTGACT | 2880 |
| TCTGACCAAC | AGAGTGTGGG | GAGAAGGGAT | GTGTATTAGC | CCCGGAGGAC | GTGATGTGAG | 2940 |
| ACCCGCTTGT | GAGTCCTCCA | CACTCGTTCC | CCATTGGCAA | GATACATGGA | GAGCACCTTG | 3000 |

AGGACCTTTA AAAGGCAAAG CCGCAAGGCA GAAGGAGGCT GGGTCCCTGA ATCACCGACT 3060
GGAGGAGAGT TACCTACAAG AGCCTTCATC CAGGAGCATC CACACTGCAA TGATATAGGA 3120
WTGAGGTCTG AACTCCACTG AATTAAACCA CTGGCATTG GGGGCTGTTC ATTATAGCAG 3180
TGCAAAGAGT TCCTTTATCC TCCCCAAGGA TGGAAAATAC AATTTATTTT GCTTACCATA 3240
CACCCCTTTT CTCTTCGTCC ACATTTTCCA ATCTGTATGG TGGCTGTCTT CTATGGCAGA 3300
AGGTTTGGG GAATAAATAG CGTGAAATGC TAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3360
AAAAAA 3367

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Met Gly Arg Pro Leu Leu Pro Leu Leu Leu Leu Gln Pro Pro
1 5 10 15
Ala Phe Leu Gln Pro Gly Gly Ser Thr Gly Ser Gly Pro Ser Tyr Leu
20 25 30
Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser
35 40 45
Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala
50 55 60
Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
65 70 75 80
Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
85 90 95
Leu Phe Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu Arg Ile
100 105 110
Ser Asn Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
115 120 125
Leu Asp Thr Arg Arg Ser Gly Arg Gln Gln Leu Gln Ser Ile Lys Gly
130 135 140
Thr Lys Leu Thr Ile Thr Gln Ala Val Thr Thr Thr Thr Trp Thr
145 150 155 160

Pro Ser Ser Thr Thr Thr Ile Ala Gly Leu Arg Val Thr Glu Ser Lys
165 170 175

Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Ile Arg Val
180 185 190

Ala Leu Ala Val Ala Val Leu Lys Thr Val Ile Leu Gly Leu Leu Cys
195 200 205

Leu Leu Leu Trp Trp Arg Arg Arg Lys Gly Ser Arg Ala Pro Ser Ser
210 215 220

Asp Phe
225

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3899 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

| | |
|---|-----|
| GGGAAGAGAT GGTGACTGAG GCAGAAGCTA ATAGGGAAGA TGATAGGAAA GAAATTTTAC | 60 |
| CCAAGGGAAT TAGATTTAGC AAGAGAGCGA AGGAAAGCTG AGAGGCCAAA AACATCTCTG | 120 |
| AGGAAACTG ACTCTGAGAG AGAAGAGGTG ACAAGGGCAA ATGCACTCAA GGATGAAGAT | 180 |
| GCTTTTAAAG AAGAGCAAAA ACTTAAAGCG GAAGAAGGGG AAACAGAGAC AGAAGTWAGA | 240 |
| GCTGAGGAAG AGACAAAAGC TCCCCCAAAT GAAATGGGAT CTGATGCTGA RAACGAASCA | 300 |
| CCTGTGGAGG CTTCTGAGTT GTCTGACAAT CCAGGGCTTC TAGGAGAARA TTACTATAAA | 360 |
| GAGACAGTGG TTCCCATATT TGAAGCAACG CCTGGATTTC AAAAGTCGCT GGAAAACATA | 420 |
| ACAGCTCTGA GGAAAGAAGG AGGAGGGGAA AGACTGAGTG AAGCCAGAGA CACAGAGCAC | 480 |
| AAAGACAGAG AAGAGCTGTC CAGCAGGGAG AATAGGGCCC TGAAGGAAGG GCACCGCCAA | 540 |
| GATGGAGAGG GGGCCTTAGC AGCTCCTGAA GCTGAGCCAG CAGGAAAGGT GCAGGCCCTT | 600 |
| GAGGGGCTGA TCCCAGCCAC AGGCCAGGCA GAGGAGCTAG CAGCCAAAGA TCACGACTCC | 660 |
| TGCGCAGGAC TGGAGGGGAG AGCTGAAGGG CAAGGAGGAG TGGATGTCGT GCTAAGGACC | 720 |
| CAGGAAGCTG TTGCTGAGGA AGATCCCATA WTGGCAGAAA AGTTCAGGGA GGAAGCGGTG | 780 |
| GATGAGGACC CAGAGGAGGA AGAGGACAAA GAGTGCAATC TGGAGACAGA AGCGATGCAG | 840 |

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|------|
| GACAGGAACT | CGGAAGGGGA | CGGGGACATG | GAAGGAGAAG | GAAACACACA | AAAGAATGAG | 900 |
| GGCATGGGAG | GAGGAAGGGT | TGTGGCTGTG | GAAGTTCTAC | ACGGAGGTGG | TGAAACGGCA | 960 |
| GAAACAGCCG | CAGAGGAGAG | GGAGGTGTTG | GCAGGTTTCG | AGACAGCCGA | GGAGAAAACA | 1020 |
| ATAGCAAATA | AAGCCTCCTC | CTTTTCAGAT | GTTGCTGAGG | AAGAAACCTG | GCACCAACAG | 1080 |
| GATGAGTTAG | TAGGAAAAAC | AGCAGCTGCA | GGGAAGGTGG | TGGTAGAGGA | ATTAGCACGG | 1140 |
| AGTGGGGAGG | AAGTGCCAGC | AGCAGAGGAG | ATGACAGTGA | CATATACAAC | AGAGGCTGGG | 1200 |
| GTGGGCACTC | CAGGAGCCCT | GGAGCGGAAG | ACCTCAGGGC | TAGGACAGGA | GCAAGAGGAA | 1260 |
| GGGTCAGAGG | GCCAGGAGGC | AGCCACTGGG | AGTGGCGATG | GGAGGCAGGA | GACAGGAGCA | 1320 |
| GCTGAAAAAT | TCCGATTAGG | ATTATCACGG | GAGGGAGAGA | GGGAATTGAG | TCCGGAGAGT | 1380 |
| CTACAGGCGA | TGGCAACACT | TCCAGTGAAG | CCTGATTTC | CTGAAACCCG | AGAGAAGCAA | 1440 |
| CAGCATATGG | TGCAAGGAGA | AAGCGAGACT | GCAGATGTTT | CCCCCAACAA | CATGCAGGTC | 1500 |
| TAGGAGACTT | GCTGGCAGAC | GGATAATTTA | AAGATGTCTT | CTGAAGATGT | AAAGAGTGGA | 1560 |
| GAAAGATTCA | CGCAAGCATC | TCACCAGGAT | TCTTGATTTT | CTCTCTCTCC | TCTTTAGTTG | 1620 |
| CTGGTTGCGC | TTGTCTGAGA | TGATJCCCAA | TCTGTCAGCC | CTGGTCAGTA | GCTCAGTAAG | 1680 |
| CACCTTGAGA | ATAGCTCAAG | TAGATCTGTA | GGACCCTTCT | TAGAAGCAGT | GGTTCCTCAT | 1740 |
| GGAGAACTT | GTGAGGCTGT | TACACATTCT | ACACACCTAA | CATTATTTTC | AAACAAAAAT | 1800 |
| GATAATTTTC | AGATGCTTGA | CTTTTACCAA | AGATCACTGG | AAGGCCCAGT | CCTAATGTTA | 1860 |
| GGGGTTTGTT | TAAAGTCCTT | TTTATTTTAC | AATACAGAGC | CCCAGTCAAT | TCCACAATCT | 1920 |
| CAATTTCATA | CATGGGAATT | TTATTTAAAA | ATCTGTGGTT | TGGGGCTTTA | ATGAATTGGC | 1980 |
| CTGTGAAAAT | GAGCTCTAAA | TTTCCTCCCA | CGTACACTCA | AAACTCAAGA | TTGCTCCAAA | 2040 |
| TCTCTAAGTT | CTTCCAGCAA | AAGATTTCTT | GGCATGTATA | TTCACCTATA | CTTAGAAATA | 2100 |
| TTCATTCTTT | TAATTTATGC | CAGAATAACA | AAGTGGAAT | CTTATTTCAA | AATGCTCTTT | 2160 |
| GTTTTTTTGT | GTGTGTTTCT | GTAGTTCTGC | TTTCTGGGGT | AGACTAGTAA | AATGGTAGCT | 2220 |
| TCCAGCATTT | TGTCCCTGGG | GCCTTCTTTA | TAGGGCCACT | CAAATTTAAA | TAAAAGTAGT | 2280 |
| AAATAATTTA | GCTAAGTGGA | ATAAGTATAA | TAATTATAGT | GGTAAGCATA | GCACATCAGC | 2340 |
| ATTATGCCAA | CATTCTAGAC | TCTTTAGTTG | ATGTCATTAA | ATGGAAAAGA | AACCTGGATT | 2400 |
| AAATGAGTGT | GCTGCTCACC | TTCCCAAGTT | CTGTTATTTT | AAACCTGTGA | ACTAACCTTG | 2460 |
| CAGTTCATTA | TAAATCAACA | GTAACAACCTG | CATTCTAAAT | TACTCCCTGA | TATTATTTTC | 2520 |

| | |
|---|------|
| TAGTTGTGTA TCAGCCTGTC TCCTAGGGGT TTTCATTTCC CTGAAGACAT ACAAGTGCCC | 2580 |
| CAGAGCGCAT GTATATGTCT ACCATTTCTC TATATGAGAA GGTAAAAAAA ATTTCTTTAA | 2640 |
| GCAGTGATTT TCCAGCCAGA ATATACATTA GATTTTCATG GGACGCTTTT ATAAATGACT | 2700 |
| CAACCCCTTTT CCCCACCCCA GAGATTCAGA CTTAATTCGT TTTAGATGGA TCTACACATC | 2760 |
| AGTATATATA TATTTTAAAC TTTTCACTTG ATTCTTCTCT GTAGCCAAGG TTGAGAACCG | 2820 |
| CTGTTCTAAA TCATCATATA ATCCATGCTG GCCACATTAC ACTCAAGGTC CCTAGGGACC | 2880 |
| AGGCATATTA TCATAGTAGG TATCTTCCAT TTTAATGTGT AATGGAGCCA TTCAATGATC | 2940 |
| AAAAATACAC TGGACCAGAT AGTAGACTGG TCCCTTGATC AGAAGCATCA GCACATCAGC | 3000 |
| ATCACCTGGA AATTGTTCCC AGCCTTTGTC TCCTACCTAC TAAATTAGAA ACTCTTGGTG | 3060 |
| GGTTCAGTA ATCCATAGCT TAACAAGCCC TGCAGTTAAT ACTGATGTAC ACTGATGTCC | 3120 |
| AAAAACTGCT GTCATGGACT ATTGATTGTA TTGAGGATTA GTCTCAGTTG GAAAGCCAAC | 3180 |
| TACAGAGGCA TTTTGAACCT TCTTTCTTTG CCTCTCTATG TCTCTCTGTC TTTTCTTGTC | 3240 |
| TTCTGATTTA TCTGTCTTTC TTTCTCTAGT AAATGGCACT CAATATAAAA GTGGTGGAGT | 3300 |
| CAATCTTAAA CTTATTTTTA TTATGATTGT ATTGATACAT GCACGAAGTC CCTCTGCCCT | 3360 |
| ACTCCCTATT CAAGGATATT ACTCACTGCA CATCATAAAT CTCCATCATC TGTCTTAAAG | 3420 |
| TTTTATGAGT AGATTTTCATC TACATTATAT TCAAGTTCAT TTATTACTGA GCTGTATTAC | 3480 |
| TGTGGAGCTC TAACAGTATT TGTTTCCTGA TTTCAAATC AATGCTACAG AGCAC'TTTGA | 3540 |
| ATACATCACA CCTTATAGGA AAGATAGTAA ATGTATTAAT CCCATTGAAA AATTAGTTTT | 3600 |
| GTACAATGTG CTAAATAGTA TTGCATTGGA TTACTTTTAT ATTTAACACA CTCCATCAAA | 3660 |
| ACATCCCATATA ACATAATTTT ACAATCTGCA TGTGAATTTA ACTGTGAAAT TCAGTATTGT | 3720 |
| GATATTTTGA ATAAGTGAAT TCTTTCTCTG CAAATACTAT GTTGATAAAA TTACTTGTAT | 3780 |
| GTTCCCCTGA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA | 3840 |
| AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAGA | 3899 |

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Gly | Lys | Lys | Phe | Tyr | Pro | Arg | Glu | Leu | Asp | Leu | Ala | Arg | Glu | 1 | 5 | 10 | 15 |
| Arg | Arg | Lys | Ala | Glu | Arg | Pro | Lys | Thr | Ser | Leu | Arg | Lys | Thr | Asp | Ser | 20 | 25 | 30 | |
| Glu | Arg | Glu | Glu | Val | Thr | Arg | Ala | Asn | Ala | Leu | Lys | Asp | Glu | Asp | Ala | 35 | 40 | 45 | |
| Phe | Lys | Glu | Glu | Gln | Lys | Leu | Lys | Ala | Glu | Glu | Gly | Glu | Thr | Glu | Thr | 50 | 55 | 60 | |
| Glu | Val | Arg | Ala | Glu | Glu | Glu | Thr | Lys | Ala | Pro | Pro | Asn | Glu | Met | Gly | 65 | 70 | 75 | 80 |
| Ser | Asp | Ala | Glu | Asn | Glu | Xaa | Pro | Val | Glu | Ala | Ser | Glu | Leu | Ser | Asp | 85 | 90 | 95 | |
| Asn | Pro | Gly | Leu | Leu | Gly | Glu | Xaa | Ser | Leu | Lys | Glu | Thr | Val | Val | Pro | 100 | 105 | 110 | |
| Ile | Phe | Glu | Ala | Thr | Pro | Gly | Phe | Glu | Lys | Ser | Leu | Glu | Asn | Ile | Thr | 115 | 120 | 125 | |
| Ala | Leu | Arg | Lys | Glu | Gly | Gly | Gly | Glu | Arg | Leu | Ser | Glu | Ala | Arg | Asp | 130 | 135 | 140 | |
| Thr | Glu | His | Lys | Asp | Arg | Glu | Glu | Leu | Ser | Ser | Arg | Glu | Asn | Arg | Ala | 145 | 150 | 155 | 160 |
| Leu | Lys | Glu | Gly | His | Arg | Gln | Asp | Gly | Glu | Gly | Ala | Leu | Ala | Ala | Pro | 165 | 170 | 175 | |
| Glu | Ala | Glu | Pro | Ala | Gly | Lys | Val | Gln | Ala | Pro | Glu | Gly | Leu | Ile | Pro | 180 | 185 | 190 | |
| Ala | Thr | Gly | Gln | Ala | Glu | Glu | Leu | Ala | Ala | Lys | Asp | His | Asp | Ser | Cys | 195 | 200 | 205 | |
| Ala | Gly | Leu | Glu | Gly | Arg | Ala | Glu | Gly | Gln | Gly | Gly | Val | Asp | Val | Val | 210 | 215 | 220 | |
| Leu | Arg | Thr | Gln | Glu | Ala | Val | Ala | Glu | Glu | Asp | Pro | Ile | Xaa | Ala | Glu | 225 | 230 | 235 | 240 |
| Lys | Phe | Arg | Glu | Glu | Ala | Val | Asp | Glu | Asp | Pro | Glu | Glu | Glu | Glu | Asp | 245 | 250 | 255 | |
| Lys | Glu | Cys | Xaa | Leu | Glu | Thr | Glu | Ala | Met | Gln | Asp | Arg | Asn | Ser | Glu | 260 | 265 | 270 | |
| Gly | Asp | Gly | Asp | Met | Glu | Gly | Glu | Gly | Asn | Thr | Gln | Lys | Asn | Glu | Gly | 275 | 280 | 285 | |

Met Gly Gly Gly Arg Val Val Ala Val Glu Val Leu His Gly Gly Gly
290 295 300

Glu Thr Ala Glu Thr Ala Ala Glu Glu Arg Glu Val Leu Ala Gly Ser
305 310 315 320

Glu Thr Ala Glu Glu Lys Thr Ile Ala Asn Lys Ala Ser Ser Phe Ser
325 330 335

Asp Val Ala Glu Glu Glu Thr Trp His Gln Gln Asp Glu Leu Val Gly
340 345 350

Lys Thr Ala Ala Ala Gly Lys Val Val Val Glu Glu Leu Ala Arg Ser
355 360 365

Gly Glu Glu Val Pro Ala Ala Glu Glu Met Thr Val Thr Tyr Thr Thr
370 375 380

Glu Ala Gly Val Gly Thr Pro Gly Ala Leu Glu Arg Lys Thr Ser Gly
385 390 395 400

Leu Gly Gln Glu Gln Glu Glu Gly Ser Glu Gly Gln Glu Ala Ala Thr
405 410 415

Gly Ser Gly Asp Gly Arg Gln Glu Thr Gly Ala Ala Glu Lys Phe Arg
420 425 430

Leu Gly Leu Ser Arg Glu Gly Glu Arg Glu Leu Ser Pro Glu Ser Leu
435 440 445

Gln Ala Met Ala Thr Leu Pro Val Lys Pro Asp Phe Thr Glu Thr Arg
450 455 460

Glu Lys Gln Gln His Met Val Gln Gly Glu Ser Glu Thr Ala Asp Val
465 470 475 480

Ser Pro Asn Asn Met Gln Val
485

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 483 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CATTGCTAGA CAGACTCTCT TGCTTGGATG GTACTCCACC ACTTTCTTGG CACATGAGAT 60

GCAAGATTGC TCAGGGTGCA GCTAATGGCA TCAATTTTCT ACATGAAAAT CATCATATTC 120

ATAGAGATAT TAAAAGTGCA AATATCTTAC TGGATGAAGC TTTTACTGCT AAAATATCTG 180
 ACTTTGGCCT TGCACGGGCT TCTGAGAAAGT TTTGCCCAGA CAGTCATGAC TAGCAGAATT 240
 GTGGGAACAA CAGCTTATAT GGCACCAGAA GCTTTGCGTG GAGAAATAAC ACCCAAATCT 300
 GATATTTACA GCTTTGGTGT GGTTTTACTA GAAATAATAA CTGGACTTCC AGCTGTGGAT 360
 GAACACCGTG AACCTCAGTT ATTGCTAGAT ATTAAAGAAG AAATTGAAGA TGAAGAAAAG 420
 ACATTGAAGA TTATATTGAT AAAAAGATGA ATGATGCTGA TTCCAATTCA GTTGAAGCTA 480
 TGT 483

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Ala Ser Ile Phe Tyr Met Lys Ile Ile Ile Phe Ile Glu Ile Leu
 1 5 10 15
 Lys Val Gln Ile Ser Tyr Trp Met Lys Leu Leu Leu Leu Lys Tyr Leu
 20 25 30
 Thr Leu Ala Leu His Gly Leu Leu Arg Ser Phe Ala Gln Thr Val Met
 35 40 45
 Thr Ser Arg Ile Val Gly Thr Thr Ala Tyr Met Ala Pro Glu Ala Leu
 50 55 60
 Arg Gly Glu Ile Thr Pro Lys Ser Asp Ile Tyr Ser Phe Gly Val Val
 65 70 75 80
 Leu Leu Glu Ile Ile Thr Gly Leu Pro Ala Val Asp Glu His Arg Glu
 85 90 95
 Pro Gln Leu Leu Leu Asp Ile Lys Glu Glu Ile Glu Asp Glu Glu Lys
 100 105 110
 Thr Leu Lys Ile Ile Leu Ile Lys Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

| | |
|--|-----|
| AATCTGAGTC AGCTTAGAAG ATANTCCAAG CTTTCAGATGA TAACCACAGC CTGGGCTGAC | 60 |
| ACCTGGATTT CAGCTTTGCA TGATCCTCAG TATGAGAATC TATCTGTTCT GTGCTGGACT | 120 |
| TCTAATATAT AGAACTGTGA GATAATGGGT CACATTGGCT GGATGTGGTG GCTCATACCT | 180 |
| GTAAATCCCA GCACTTTGGG AGGCCGAGGC AGGCAGATCA CCTGAGGTCA GGAGTTCAAG | 240 |
| ACCGGCCTGG CCAGCATGGT GAAGCCCCGT CTTTACTAGA AATACAAAAA TTAGACGAGC | 300 |
| GTGGTGGTGG ACACCTGTGT TCCCAGCTAC TTGGGAGGCT GAGGCAGGAG ACTGGCTGGA | 360 |
| ACCAGGGAGG TAGAGGTTGC AGTGAGCTGA GATCGTGCCA CTGCACTCCA GCCTGGGTGA | 420 |
| CAGAGTGAGA CTCCATCATA AATAAATAAA TAAATAAATG GGTCACATTA AGCCTTTAAA | 480 |
| AAAAAAAAAA AAA | 493 |

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2682 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

| | |
|---|-----|
| GGTTCACAGA AGAGTTTGCG ACGTGGTAAA GAAATAAGGC GAGTACACAA GCGAAGACTT | 60 |
| TCCAGCTCAG AGAGTGAAGA GAGCTATTTG TCCAAGAAGT CTGAAGATGA TGAGCTAGCT | 120 |
| AAAGAATCAA AGCGGTCAGT TCGAAAGCGG GGCCGAAGCA CAGACGAGTA TTCAGAAGCA | 180 |
| GATGAGGAGG AGGAGGAAGA RGAAGGCAAA CCATCCCGCA AACGGCTACA CCGGATTGAG | 240 |
| ACGGATGAGG ARGAGAGTTG TGACAATGCT CATGGAGATG CAAATCAGCC TGCCCGTGAC | 300 |
| AGCCAGCCTA GGGTCCTGCC CTCAGAACAA GAGAGCACCA AGAAGCCCTA CCGGATAGAA | 360 |
| AGTGATGAGG AAGAGGACTT TGAAAATGTA GGCAAAGTGG GGAGCCCATT GGACTATAGC | 420 |
| TTAGTGGAAT TACCTTCAAC CAATGGACAG AGCCCTGGCA AAGCCATTGA GAACTTGATT | 480 |

| | | | | | | |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| GGCAAGCCTA | CTGAGAAGTC | TCAGACCCCC | AAGGACAACA | GCACAGCCAG | TGCAAGCCTA | 540 |
| GCYTCCCAAT | GGGACAAGTG | GTGGGCAGGA | GGCAGGAGCA | CCAGAAGAGG | AGGAAGATGA | 600 |
| GCTTTTGAGA | GTGACTGACC | TTGTTGATTA | TGTCTGTAAC | AGTGAACAGT | TATAAGACTT | 660 |
| TTTTTCCATT | TTTGTGCTAA | TTTATTCCAC | GGTAGCTCTC | ACACCAGCGG | GCCAGTTATT | 720 |
| AAAAGCTGTT | TAATTTTTTCC | TAGAAAACTC | CACTACAGAA | TGACTTTTAT | AAGAAAAATT | 780 |
| TCAACAAATC | CTGAAGTCTT | TCTGTGAAGT | GACCAGTTCT | GAACCTTGAA | GATAAATAAT | 840 |
| TGCTGTAAAT | TCCTTTTGAT | TTTCTTTTTC | CAGGTTTCATG | GTCCTTGGTA | ATTTCAATTCA | 900 |
| TGGAAAAAAA | TCTTATTATA | ATAACAACAA | AGATTGTAT | ATTTTTGACT | TTATATTTCC | 960 |
| TGAGCTCTCC | TGACTTTGTG | AAAAAGGGTG | ATGAAAATGC | ATTCCGAATC | TGTGAGGGCC | 1020 |
| CAAAACAGAA | TTTAGGGGTG | GGTGAAAGCA | CTTGTGCTTT | AGCTTTTTCA | TATTAAATAT | 1080 |
| ATATTATATT | TAAACATTCA | TGGCATAGAT | GATGATTTAC | AGACAATTTA | AAAGTTCAAG | 1140 |
| TCTGTACTGT | TACAGTTTGA | GAATTGTAGA | TAACATCATA | CATAAGTCAT | TTAGTAACAG | 1200 |
| CCTTTGTGAA | ATGAACTTGT | TTACTATTGG | AGATAACCAC | ACTTAATAAA | GAAGAGACAG | 1260 |
| TGAAAGTACC | ATCATAATTA | ACCTAAATTT | TTGTTATAGC | AGAGTTTCTT | GTTTAAAAAA | 1320 |
| AAAWAAAWG | CRKCYGMAAA | GCATTTGTAC | AGTAAAATGT | ATAATGAAGC | TTTGCCAACC | 1380 |
| AGACTGTGCT | AGCAACAAAT | TTTTTTAAAT | AAGCTTTATG | CAGTGGAAT | AAGGTGGCCT | 1440 |
| CAAATATATT | GTGTCTGATG | GAGAGTTATT | AGTGAAATGA | ATGTGGTCTT | TCTTAAGGCC | 1500 |
| TGGGTGGACT | GTAAACTTTG | CCAATAGTAT | AACTCTTGTC | TTCTGGCCAC | TTGATGTTTA | 1560 |
| AATATCTGAA | ATATCATTTT | GAAAAAATA | CATCTATATA | TAACATACAT | GAAGAGATGC | 1620 |
| TAAGCTGACA | GTGATATTTT | AGCACATTTG | AAGACTGGGA | AGAGATTTTC | AGGTGAATTT | 1680 |
| TAAGTGGTCT | ATTCTTGCCC | TTAGTATCTA | CTTCAAATTG | AAGTCTACAA | ACAAAGCAGT | 1740 |
| TCCTTTGGGA | GGTTTTTAGT | TTGAGTTTTA | GCGTGTGTGT | GTGTTTGTGT | GTGTGCGTGT | 1800 |
| GCGTGTGTGT | GTGTGTTGGA | ATTCCTATC | TGCCTGGATA | TATTAGCAGA | GTTTGAATGT | 1860 |
| AGTTTTGGCC | TTTGGCCATT | AGACTTCTAT | TAAAATTCAT | TAATAGTCAT | ACAACCAACA | 1920 |
| TAGAGTTGAA | TGAGAACTGC | CGATGTAATT | AATAGGCATG | ACATCCATTT | CAAACATCTC | 1980 |
| AACACTTTAA | AGAAAAGCCC | TTTGTTTCAA | GAAAAAAGGG | TTTGTAACATA | ACTAAATACC | 2040 |
| TAACATGTAA | TTGACACTAA | AATATGAACT | TTGTCTTATT | TAGTTTCTGT | TATAGCTGTA | 2100 |
| AAATTTTCAGG | CAGAGCCATA | ACATTGTACA | GAGTGTAGCA | CTTGTGATTA | AACCTAGCCT | 2160 |
| GTAAATCCT | GAAACCTTCA | ACCATTACTT | CTGTGAATAC | TTTAGCCCTG | GGATTTGGGT | 2220 |

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TTTTCTGTTC CGGTGTTGTG TCTGTTGCCG GCAATGGACA CACCATATCT GCTGCTGGCC      2280
CAAGGAACGT CATTAATTTT TCTTTCCAAA TTAAGTATTA TGTGCTAGTC AGTGTATAGT      2340
AAAGCACTTC TCTTTTTTAT TACTAAAAAG CTGGCATTAG ATTTGCATTA TAAATACCTC      2400
TCTAGGAACT TTATACTCCT TTCCTTCTT CAACAGGTAT TGCCCTTAAA TCTTATCTTT      2460
TGGCCTTGAA AGTTTATAGC TATTGTTTTT CAGTTGTTCG TTGTTTTGTT TTGTTTCACT      2520
TTAGTTCTGT AGTACCTGCC CATTAATATT TTTGCTTTGA TTCTAGCAAT GTGTATGTAT      2580
CTGTATAAAA AATAAAATAA TGAAAGCAAC CTAAAAATAG GATGCACCAA TTAAAAAAA      2640
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA                          2682

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(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

```

Met Glu Lys Asn Leu Ile Ile Ile Thr Thr Lys Ile Cys Ile Phe Leu
 1              5              10              15
Thr Leu Tyr Phe Leu Ser Ser Pro Asp Phe Val Lys Lys Gly Asp Glu
          20              25              30
Asn Ala Phe Arg Ile Cys Glu Gly Pro Lys Gln Asn Leu Gly Val Gly
          35              40              45
Glu Ser Thr Cys Ala Leu Ala Phe Ser Tyr
 50              55

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(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2522 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCCGAGCGCC CGCGCCGCCG CTGCCTCTGT CCTCCGCGCG CTGCTCAGCT GAAGGCGCAC 60

AGGATTCAAT TACTGGACTT GTCAACTCTG CCAGTGACG TGCCATTTCT CTTCCACTAT 120

GAGAGGACCG ATTGTATTGC ACATTTGTCT GGCTTTCTGT AGCCTTCTGC TTTTCAGCGT 180

TGCCACACAA TGTCTGGCCT TCCCCAAAAT AGAAAGGAGG AGGGAGATAG CACATGTTCA 240

TGCGGAAAAA GGGCAGTCCG ATAAGATGAA CACCGATGAC CTAGAAAATA GCTCTGTTAC 300

CTCAAAGCAG ACTCCCCAAC TGGTGGTCTC TGAAGATCCA ATGATGATGT CAGCAGTACC 360

ATCGGCAACA TCATTAAATA AAGCATTCTC GATTAACAAA GAAACCCAGC CTGGACAAGC 420

TGGGCTCATG CAAACAGAAC GCCCTGGTGT TTCCACACYT ACTGAGTCAG GTGTCCCCTC 480

AGCTGAAGAA GTATTTGGTT CCAGCCAGCC AGAGAGAATA TCTCCTGAAA GTGGACTTGC 540

CAAGGCCATG TTAACCATTG CTATCACTGC GACTCCTTCT CTGACTGTTG ATGAAAAGGA 600

GGAACTCCTT ACAAGCACTA ACTTTCAGCC CATTGTAGAA GAGATCACAG AAACCACAAA 660

AGGTTTTCTG AAGTATATGG ATAATCAATC ATTTGCAACT GAAAGTCAGG AAGGAGTTGG 720

TTTGGGACAT TCACCTTCAT CCTATGTGAA TACTAAGGAA ATGCTAACCA CCAATCCAAA 780

GACTGAGAAA TTTGAAGCAG ACACAGACCA CAGGACAAC TCTTTTCCTG GTGCTGAGTC 840

CACAGCAGGC AGTGAGCCTG GAAGCCTCAC CCCTGATAAG GAGAAGCCTT CGCAGATGAC 900

AGCTGATAAC ACCCAGGCTG CTGCCACCAA GCAACCACTC GAAACTTCCG AGTACACCCT 960

GAGTGTTGAG CCAGAACTG ATAGTCTGCT GGGAGCCCCA GAAGTCACAG TGAGTGTCAG 1020

CACAGCTGTT CCAGCTGCCT CTGCCTTAAG TGATGAGTGG GATGACACCA AATTAGAGAG 1080

TGTAAGCCGG ATAAGGACCC CCAAGCTTGG AGACAATGAA GAGACTCAGG TGAGAACGGA 1140

GATGTCTCAG ACAGCACAAG TAAGCCATGA GGGTATGGAA GGAGGCCAGC CTTGGACAGA 1200

GGCTGCACAG GTGGCTCTGG GGCTGCCTGA AGGGGAAACA CACACGGGCA CAGCCCTGCT 1260

AATAGCGCAT GGGAATGAGA GATCACCTGC TTTCACTGAT CAAAGTTCCT TTACCCCCAC 1320

AAGTCTGATG GAAGACATGA AAGTTTCCAT TGTGAACTTG CTCAAAGTA CGGGAGACTT 1380

CACGGAATCC ACCAAGGAAA ACGATGCCCT GTTTTTCTTA GAAACCACTG TTTCTGTCTC 1440

TGTATATGAG TCTGAGGCAG ACCAACTGTT GGGAAATACA ATGAAAGACA TCATCACTCA 1500

AGAGATGACA ACAGCTGTTC AAGAGCCAGA TGCCACTTTA TCCATGGTGA CACAAGAGCA 1560

GGTTGCTACC CTCGAGCTTA TCAGAGACAG TGGCAAGACT GAGGAAGAAA AGGAGGACCC 1620

CTCTCCTGTG TCTGACGTTT CTGGTGTTAC TCAGCTGTCA AGAAGATGGG AGCCTCTGGC 1680

CACTACAATT TCAACTACAG TCGTCCCTTT GTCTTTTGAA GTTACTCCCA CTGTGGAAGA 1740

ACAAATGGAC ACAGTCACAG GGCCAAATGA GGAGTTCACA CCAGTTCTGG GATCTCCAGT 1800
 GACACCTCCT GGAATAATGG TGGGGGAACC CAGCATTTC CCTGCACTTC CTGCTTTGGA 1860
 GGCATCCTCT GAGAGAAGAA CTGTTGTTCC ATCTATTACT CGTGTTAATA CAGCTGCCTC 1920
 ATATGGCCTG GACCAACTTG AATCTGAAGA GGGACAAGAA GATGAGGATG AAGAGGATGA 1980
 AGAAGATGAA GATGAAGAAG AGGAAGATGA GGAAGAAGAT GAGGAAGATA AAGATGCAGA 2040
 CTCGCTGGAT GAGGGCTTGG ATGGTGACAC TGAGCTGCCA GGTTTTACCC TCCCTGGTAT 2100
 CACATCCCAG GAACCAGGCT TAGAGGAGGG AAACATGGAC CTGTTGGAGG GAGCTACCTA 2160
 CCAGGTGCCA GATGCCYTCG AGTGGGAACA GCAGAATCAA GGCCTGGTGA GAAGCTGGAT 2220
 GGAAAAATTM AAAGACAAGG CTGGTTACAT GTCTGGGATG CTGGTGCCTG TAGGGGTTGG 2280
 GATAGCTGGA GCCTTGTTCA TCTTGGGAGC CCTCTACAGC ATTAAGGTTA TGAATCGCCG 2340
 AAGGAGAAAT GGCTTCAAAA GGCATAAAAG AAAGCAGAGA GAATTCAACA GCATGCAAGA 2400
 TCGAGTAATG CTCTTAGCCG ACAGCTCTGA AGATGAATTT TGAATTGGAC TGGGTTTTAA 2460
 TTGGGATATT CAACGATGCT ACTATTCTAA TTTTATTTT GGAGCAGAAA AAAAAAAAAA 2520
 AA 2522

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Met Arg Gly Pro Ile Val Leu His Ile Cys Leu Ala Phe Cys Ser Leu
 1 5 10 15
 Leu Leu Phe Ser Val Ala Thr Gln Cys Leu Ala Phe Pro Lys Ile Glu
 20 25 30
 Arg Arg Arg Glu Ile Ala His Val His Ala Glu Lys Gly Gln Ser Asp
 35 40 45
 Lys Met Asn Thr Asp Asp Leu Glu Asn Ser Ser Val Thr Ser Lys Gln
 50 55 60
 Thr Pro Gln Leu Val Val Ser Glu Asp Pro Met Met Met Ser Ala Val
 65 70 75 80

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ser | Ala | Thr | Ser | Leu | Asn | Lys | Ala | Phe | Ser | Ile | Asn | Lys | Glu | Thr | 85 | 90 | 95 | |
| Gln | Pro | Gly | Gln | Ala | Gly | Leu | Met | Gln | Thr | Glu | Arg | Pro | Gly | Val | Ser | 100 | 105 | 110 | |
| Thr | Xaa | Thr | Glu | Ser | Gly | Val | Pro | Ser | Ala | Glu | Glu | Val | Phe | Gly | Ser | 115 | 120 | 125 | |
| Ser | Gln | Pro | Glu | Arg | Ile | Ser | Pro | Glu | Ser | Gly | Leu | Ala | Lys | Ala | Met | 130 | 135 | 140 | |
| Leu | Thr | Ile | Ala | Ile | Thr | Ala | Thr | Pro | Ser | Leu | Thr | Val | Asp | Glu | Lys | 145 | 150 | 155 | 160 |
| Glu | Glu | Leu | Leu | Thr | Ser | Thr | Asn | Phe | Gln | Pro | Ile | Val | Glu | Glu | Ile | 165 | 170 | 175 | |
| Thr | Glu | Thr | Thr | Lys | Gly | Phe | Leu | Lys | Tyr | Met | Asp | Asn | Gln | Ser | Phe | 180 | 185 | 190 | |
| Ala | Thr | Glu | Ser | Gln | Glu | Gly | Val | Gly | Leu | Gly | His | Ser | Pro | Ser | Ser | 195 | 200 | 205 | |
| Tyr | Val | Asn | Thr | Lys | Glu | Met | Leu | Thr | Thr | Asn | Pro | Lys | Thr | Glu | Lys | 210 | 215 | 220 | |
| Phe | Glu | Ala | Asp | Thr | Asp | His | Arg | Thr | Thr | Ser | Phe | Pro | Gly | Ala | Glu | 225 | 230 | 235 | 240 |
| Ser | Thr | Ala | Gly | Ser | Glu | Pro | Gly | Ser | Leu | Thr | Pro | Asp | Lys | Glu | Lys | 245 | 250 | 255 | |
| Pro | Ser | Gln | Met | Thr | Ala | Asp | Asn | Thr | Gln | Ala | Ala | Ala | Thr | Lys | Gln | 260 | 265 | 270 | |
| Pro | Leu | Glu | Thr | Ser | Glu | Tyr | Thr | Leu | Ser | Val | Glu | Pro | Glu | Thr | Asp | 275 | 280 | 285 | |
| Ser | Leu | Leu | Gly | Ala | Pro | Glu | Val | Thr | Val | Ser | Val | Ser | Thr | Ala | Val | 290 | 295 | 300 | |
| Pro | Ala | Ala | Ser | Ala | Leu | Ser | Asp | Glu | Trp | Asp | Asp | Thr | Lys | Leu | Glu | 305 | 310 | 315 | 320 |
| Ser | Val | Ser | Arg | Ile | Arg | Thr | Pro | Lys | Leu | Gly | Asp | Asn | Glu | Glu | Thr | 325 | 330 | 335 | |
| Gln | Val | Arg | Thr | Glu | Met | Ser | Gln | Thr | Ala | Gln | Val | Ser | His | Glu | Gly | 340 | 345 | 350 | |
| Met | Glu | Gly | Gly | Gln | Pro | Trp | Thr | Glu | Ala | Ala | Gln | Val | Ala | Leu | Gly | 355 | 360 | 365 | |
| Leu | Pro | Glu | Gly | Glu | Thr | His | Thr | Gly | Thr | Ala | Leu | Leu | Ile | Ala | His | 370 | 375 | 380 | |

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Asn | Glu | Arg | Ser | Pro | Ala | Phe | Thr | Asp | Gln | Ser | Ser | Phe | Thr | Pro | 385 | 390 | 395 | 400 |
| Thr | Ser | Leu | Met | Glu | Asp | Met | Lys | Val | Ser | Ile | Val | Asn | Leu | Leu | Gln | 405 | 410 | 415 | |
| Ser | Thr | Gly | Asp | Phe | Thr | Glu | Ser | Thr | Lys | Glu | Asn | Asp | Ala | Leu | Phe | 420 | 425 | 430 | |
| Phe | Leu | Glu | Thr | Thr | Val | Ser | Val | Ser | Val | Tyr | Glu | Ser | Glu | Ala | Asp | 435 | 440 | 445 | |
| Gln | Leu | Leu | Gly | Asn | Thr | Met | Lys | Asp | Ile | Ile | Thr | Gln | Glu | Met | Thr | 450 | 455 | 460 | |
| Thr | Ala | Val | Gln | Glu | Pro | Asp | Ala | Thr | Leu | Ser | Met | Val | Thr | Gln | Glu | 465 | 470 | 475 | 480 |
| Gln | Val | Ala | Thr | Leu | Glu | Leu | Ile | Arg | Asp | Ser | Gly | Lys | Thr | Glu | Glu | 485 | 490 | 495 | |
| Glu | Lys | Glu | Asp | Pro | Ser | Pro | Val | Ser | Asp | Val | Pro | Gly | Val | Thr | Gln | 500 | 505 | 510 | |
| Leu | Ser | Arg | Arg | Trp | Glu | Pro | Leu | Ala | Thr | Thr | Ile | Ser | Thr | Thr | Val | 515 | 520 | 525 | |
| Val | Pro | Leu | Ser | Phe | Glu | Val | Thr | Pro | Thr | Val | Glu | Glu | Gln | Met | Asp | 530 | 535 | 540 | |
| Thr | Val | Thr | Gly | Pro | Asn | Glu | Glu | Phe | Thr | Pro | Val | Leu | Gly | Ser | Pro | 545 | 550 | 555 | 560 |
| Val | Thr | Pro | Pro | Gly | Ile | Met | Val | Gly | Glu | Pro | Ser | Ile | Ser | Pro | Ala | 565 | 570 | 575 | |
| Leu | Pro | Ala | Leu | Glu | Ala | Ser | Ser | Glu | Arg | Arg | Thr | Val | Val | Pro | Ser | 580 | 585 | 590 | |
| Ile | Thr | Arg | Val | Asn | Thr | Ala | Ala | Ser | Tyr | Gly | Leu | Asp | Gln | Leu | Glu | 595 | 600 | 605 | |
| Ser | Glu | Glu | Gly | Gln | Glu | Asp | Glu | Asp | Glu | Glu | Asp | Glu | Glu | Asp | Glu | 610 | 615 | 620 | |
| Asp | Glu | Glu | Glu | Glu | Asp | Glu | Glu | Glu | Asp | Glu | Glu | Asp | Lys | Asp | Ala | 625 | 630 | 635 | 640 |
| Asp | Ser | Leu | Asp | Glu | Gly | Leu | Asp | Gly | Asp | Thr | Glu | Leu | Pro | Gly | Phe | 645 | 650 | 655 | |
| Thr | Leu | Pro | Gly | Ile | Thr | Ser | Gln | Glu | Pro | Gly | Leu | Glu | Glu | Gly | Asn | 660 | 665 | 670 | |
| Met | Asp | Leu | Leu | Glu | Gly | Ala | Thr | Tyr | Gln | Val | Pro | Asp | Ala | Xaa | Glu | 675 | 680 | 685 | |

Trp Glu Gln Gln Asn Gln Gly Leu Val Arg Ser Trp Met Glu Lys Xaa
690 695 700

Lys Asp Lys Ala Gly Tyr Met Ser Gly Met Leu Val Pro Val Gly Val
705 710 715 720

Gly Ile Ala Gly Ala Leu Phe Ile Leu Gly Ala Leu Tyr Ser Ile Lys
725 730 735

Val Met Asn Arg Arg Arg Arg Asn Gly Phe Lys Arg His Lys Arg Lys
740 745 750

Gln Arg Glu Phe Asn Ser Met Gln Asp Arg Val Met Leu Leu Ala Asp
755 760 765

Ser Ser Glu Asp Glu Phe
770

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2002 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

| | |
|--|-----|
| GGCAGCCCGG TACCTGAAGT CCTTCAGAAG TGCACGCCGG GACCAGGATT CCGGGAGGCC | 60 |
| GACTCCTCCC TGCCCCACGA ATGCCGGGAA TTGTGGTCTC CGCCGGACGC GAGTTGTGAG | 120 |
| ACGGCCCAAG GGGCCGCGGG GTATGCTGGG ACCGCTAGCC CTTCCGGCGC GCCTCAGGAC | 180 |
| TTCGGGTCCC CTCACCCCGG GCGGATGCCC AAAGACTCCG CCTTCCCAAG AGCCCCTGCG | 240 |
| GCCGGGCGCG AAAATGGCGG CGGCGGCGAC GGCCGGGCGC TCCTGAAGCA GCAGTTATGG | 300 |
| AGCTTCCCTC AGGGCCGGGG CCGGAGCGGC TCTTTGACTC GCACCGGCTT CCGGGTGACT | 360 |
| GCTTCCTACT GCTCGTGCTG CTGCTCTACG CGCCAGTCGG GTTCTGCCTC CTCGTCCTGC | 420 |
| GCCTGTTTCT CGGGATCCAC GTCTTCCTGG TCAGCTGCGC GCTGCCAGAC AGCGTCCTTC | 480 |
| GCAGATTCGT AGTGCGGACC ATGTGTGCGG TGCTAGGGCT CGTGGCCCGG CAGGAGGACT | 540 |
| CCGGACTCCG GGATCACAGT GTCAGGGTCC TCATTTCCAA CCATGTGACA CCTTTCGACC | 600 |
| ACAACATAGT CAATTTGCTT ACCACCTGTA GCACCGTGAG TGAGAGCGAG GCCGAGAGCG | 660 |
| CCACGGGGCG GTTCCCTGGG GCCCAGCTGA AGGCCCCCCT GTCCCCACTC GCGTTCCCCA | 720 |
| TGGAGGATAC TGAGCCTTAC CCCTAACCCC GATCCTCTAC CCAACATGTC AGTTTTTTTTT | 780 |

| | |
|--|------|
| TTCATTTTCC TCAATATTTT TCTTCTTGCT TTCTCTTCTC CTGGTTCCCA GCCTCTACTC | 840 |
| AATAGTCCCC CCAGCTTTGT GTGCTGGTCT CGGGGCTTCA TGGAGATGAA TGGGCGGGGG | 900 |
| GAGTTGGTGG AGTCACTCAA GAGATTCTGT GCTTCCACGA GGCTTCCCCC CACTCCTCTG | 960 |
| CTGCTATTCC CTGAGGAAGA GGCCACCAAT GGCCGGGAGG GGCTCCTGCG CTTCAGAGTT | 1020 |
| TGACAGTTGC CTGTTATAAG GCAGGTGTGA GCTGCTGACT AGGCTGGCTG GATTCCCATC | 1080 |
| CTACTTTCTC CTTCTCTTTC TAGTTCCTGG CCATTTTCTA TCCAAGATGT GGTACAACCT | 1140 |
| CTTACCCTGC AAGTTCAGAG ACCCCTGGTC TCTGTGACGG TGTCAGATGC CTCCTGGGTC | 1200 |
| TCAGAACTGC TGTGGTCACT TTTCGTCCCT TTCACGGTGT ATCAAGTGGC TTCGTCTGT | 1260 |
| TCATCGCCAA CTAGGGGAAG CGAATGAGGA GTTTGCACTC CGTGTACAAC AGCTGGTGGC | 1320 |
| CAAGGAATTG GGCCAGACAG GGACACGGCT CACTCCAGCT GACAAAGCAG AGCACATGAA | 1380 |
| GCGACAAAGA CACCCAGAT TGCGCCCCCA GTCAGCCCAG TCTTCTTTCC CTCCTCCCC | 1440 |
| TGGTCCTTCT CCTGATGTGC AACTGGCAAC TCTGGCTCAG AGAGTCAAGG AAGTTTGGCC | 1500 |
| CCATGTGCCA TTTGGTGTCA TCCAGAGAGA CCTGGCCAAG ACTGGCTGTG TAGACTTGAC | 1560 |
| TATCACTAAT CTGCTTGAGG GGGCCGTAGC TTTCATGCCT GAAGACATCA CCAAGGGAAC | 1620 |
| TCAGTCCCTA CCCACAGCCT CTGCCTCCAA GTTTCCCAGC TCTGGCCCCG TGACCCCTCA | 1680 |
| GCCAACAGCC CTAACATTTG CCAAGTCTTC CTGGGCCCCG CAGGAGAGCC TGCAGGAGCG | 1740 |
| CAAGCAAGCA CTATATGAAT ACGCAAGAAG GAGATTCA CA GAGAGACGAG CCCAGGAGGC | 1800 |
| TGACTGAGCT CAAAGGAACA GGATGGCACC CAGAGCCGCA GGACGGAGAC TGGGGGCAGC | 1860 |
| CCTCACCCAA CTCACAACAG GCTGGATGGG TGGGTGGTAA AAAGGGAAGG ATGAGGCTCC | 1920 |
| CCCAATGTCA CATTAAATTC ATGGTTTTCA TTCAAGGVAA AAAAAAAAAA AAAAAAAAAA | 1980 |
| AAAAAAAAAA AAAAAAAAAA AA | 2002 |

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Met Pro Pro Gly Ser Gln Asn Cys Cys Gly His Phe Ser Ser Leu Ser
1 5 10 15

Arg Cys Ile Lys Trp Leu Arg Pro Val His Arg Gln Leu Gly Glu Ala
20 25 30

Asn Glu Glu Phe Ala Leu Arg Val Gln Gln Leu Val Ala Lys Glu Leu
35 40 45

Gly Gln Thr Gly Thr Arg Leu Thr Pro Ala Asp Lys Ala Glu His Met
50 55 60

Lys Arg Gln Arg His Pro Arg Leu Arg Pro Gln Ser Ala Gln Ser Ser
65 70 75 80

Phe Pro Pro Ser Pro Gly Pro Ser Pro Asp Val Gln Leu Ala Thr Leu
85 90 95

Ala Gln Arg Val Lys Glu Val Leu Pro His Val Pro Phe Gly Val Ile
100 105 110

Gln Arg Asp Leu Ala Lys Thr Gly Cys Val Asp Leu Thr Ile Thr Asn
115 120 125

Leu Leu Glu Gly Ala Val Ala Phe Met Pro Glu Asp Ile Thr Lys Gly
130 135 140

Thr Gln Ser Leu Pro Thr Ala Ser Ala Ser Lys Phe Pro Ser Ser Gly
145 150 155 160

Pro Val Thr Pro Gln Pro Thr Ala Leu Thr Phe Ala Lys Ser Ser Trp
165 170 175

Ala Arg Gln Glu Ser Leu Gln Glu Arg Lys Gln Ala Leu Tyr Glu Tyr
180 185 190

Ala Arg Arg Arg Phe Thr Glu Arg Arg Ala Gln Glu Ala Asp
195 200 205

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CAATTGGGCC GCGAGTTGTG GTTTAAACCA GGAGTGC GCC GCGTCCGTTC ACCGCGGCCT 60

CAGATGAATG CGGCTGT TAA GACCTGCAAT AATCCAGAAT GGCTACTCTG ATCTATGTTG 120

ATAAGGAAAA TGGAGAACCA GGCACCCGTG TGGTTGCTAA GGATGGGCTG AAGCTGGGGT 180

CTGGACCTTC AATCAAAGCC TTAGATGGGA GATCTCAAGT TTCAACACCA CGTTTTGGCA 240
AAACGTTCGA TGCCCCACCA GCCTTACCTA AAGCTACTAG AAAGGCTTTG GGAAGTGTCA 300
ACAGAGCTAC AGAAAAGTCT GTAAAGACCA AGGGACCCCT CAAACAAAAA CAGCCAAGCT 360
TTTCTGCCAA AAAGATGACT GAGAAGACTG TTAAAGCAAA AAGCTCTGTT CCTGCCTCAG 420
ATGATGCCTA TCCAGAAATA GAAAAATTCT TTCCCTTCAA TCCTCTAGAC TTTGAGAGTT 480
TTGACCTGCC TGAAGAGCAC CAGATTGCGC ACCTCCCCTT GAGTGGAGTG CCTCTCWTGA 540
TCCTTGACGA GGAGAGAGAG CTTGAAAAGC TGTTTCAGCT GGGCCCCCCT TCACCTGTGA 600
AGATGCCCTC TCCACCATGG GAATCCAATC TGTTGCAGTC TCCTTCAAGC ATTCTGTCTGA 660
CCCTGGATGT TGAATTGCCA CCTGTTTGCT GTGACATAGA TATTTAAATT TCTTAGTGCT 720
TCAGAGTTTG TGTGTATTTG TATTAATAAA GCATTCTTTA ACAGAAAAAA AAAAAAAAAA 780
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 819

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Met Ala Thr Leu Ile Tyr Val Asp Lys Glu Asn Gly Glu Pro Gly Thr
1 5 10 15
Arg Val Val Ala Lys Asp Gly Leu Lys Leu Gly Ser Gly Pro Ser Ile
20 25 30
Lys Ala Leu Asp Gly Arg Ser Gln Val Ser Thr Pro Arg Phe Gly Lys
35 40 45
Thr Phe Asp Ala Pro Pro Ala Leu Pro Lys Ala Thr Arg Lys Ala Leu
50 55 60
Gly Thr Val Asn Arg Ala Thr Glu Lys Ser Val Lys Thr Lys Gly Pro
65 70 75 80
Leu Lys Gln Lys Gln Pro Ser Phe Ser Ala Lys Lys Met Thr Glu Lys
85 90 95
Thr Val Lys Ala Lys Ser Ser Val Pro Ala Ser Asp Asp Ala Tyr Pro

100

105

110

Glu Ile Glu Lys Phe Phe Pro Phe Asn Pro Leu Asp Phe Glu Ser Phe
115 120 125

Asp Leu Pro Glu Glu His Gln Ile Ala His Leu Pro Leu Ser Gly Val
130 135 140

Pro Leu
145

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

TNTCCTGCCTC AGCTGCCTCT CTGTGTAA

29

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

CNCACTGCCCT CCTTCTCCCA TAGGTACT

29

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GNAATAAGCAT GATGCTCTAC AAGGAAAG

29

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TNGGTGCCATG ATTCTGAGTG CCCTTTGC

29

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GNATATGTCAC TGTCATCTCC TCTGCTGC

29

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ANAAGCTTCAT CCAGTAAGAT ATTTGCAC

29

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ANTTCAGAACT GGTCACTTCA CAGAAAGA

29

- (2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GNATTACATA GGATGAAGGT GAATGTCC

29

- (2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ANTAGAGGCTG GGAACCAGGA GAAGAGAA

29

- (2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

TNTTGCAGGTC TTAACAGCCG CATTCATC

29

- (2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Arg Leu Pro Gly Asp Cys Phe Leu Leu Leu Val Leu Leu Leu Tyr Ala
20 25 30

Pro Val Gly Phe Cys Leu Leu Val Leu Arg Leu Phe Leu Gly Ile His
35 40 45

Val Phe Leu Val Ser Cys Ala Leu Pro Asp Ser Val Leu Arg Arg Phe
50 55 60

Val Val Arg Thr Met Cys Ala Val Leu Gly Leu Val Ala Arg Gln Glu
65 70 75 80

Asp Ser Gly Leu Arg Asp His Ser Val Arg Val Leu Ile Ser Asn His
85 90 95

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Pro | Phe | Asp | His | Asn | Ile | Val | Asn | Leu | Leu | Thr | Thr | Cys | Ser |
| | | | 100 | | | | | 105 | | | | | 110 | | |

Thr

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Ser Gln Pro Leu Leu Asn Ser Pro Pro Ser Phe Val Cys Trp Ser Arg
1 5 10 15

Gly Phe Met Glu Met Asn Gly Arg Gly Glu Leu Val Glu Ser Leu Lys
20 25 30

Arg Phe Cys Ala Ser Thr Arg Leu Pro Pro Thr Pro Leu Leu Leu Phe
35 40 45

Pro Glu Glu Glu Ala Thr Asn Gly Arg Glu Gly Leu Leu Arg Phe
50 55 60

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```

Ser Ser Trp Pro Phe Ser Ile Gln Asp Val Val Gln Pro Leu Thr Leu
1           5           10           15

Gln Val Gln Arg Pro Leu Val Ser Val Thr Val Ser Asp Ala Ser Trp
                20           25           30

Val Ser Glu Leu Leu Trp Ser Leu Phe Val Pro Phe Thr Val Tyr Gln
          35           40           45

Val
  
```

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```

CAGGTGGTCC TCCACCTGCC TTGGCTTCCT AAAGTGCTGG GATTACAGGC ATGAGTCACT      60

CTGCTGGCCT ATGTTCTGTT TTTGTTTTTG TTTTGTGTTT GAGACAGAGT TTTACTCTTG      120

TTGCCCAGGC TGGAGTGCAA TGGCATAATC TCGGCTCACT GCAGCCTCTG CCTCCCAGGT      180

TCAAGTGATT CTCCTGCCTC AGCCTCCTGA GTAGCTGGGA TTACAGGCAT GTGCCACCTC      240

ACCTGGCTAA TTTTGTATTT TTAGTAGAGA TGGGGTTTCT CCATGTTAGT CAGGCTGGTC      300

TTGAACTCCT GACCTCAGGT GATCTGCCCT CCTCAGCCTC CTAAAGTGCT GGGATTACAG      360

GTGTGAGCCA CTGTGCCCAG CCTTGTTTTT TGTTTTTTTT TTTTGTGTTT TTTTTTTGAC      420

AGTAGCCATC CTAATAGATA CTAAGTGGTA TCTCATTGTG GTTTTGATTG CATGCGTTCT      480

TTTTGGCTTG TTTTTTGAGA CAAGGTCTCA CTCCATCACC CAGACTGGAG CGCAGTGGTG      540

TGATCACGGC TCGTTGCAAC CTGACCCTCT TGAGCTCAGG TGATCCTCCC ACTTCACCCT      600

CCCGAGTATC TTGGAGTACA GGTGTGTGCC TGGCTGATTT TTCGTATTTT TTGTAGAGAT      660
  
```

| | | | | | | |
|-------------|-------------|------------|-------------|------------|-------------|------|
| GGGGTTTCAC | CGTGTGCTC | AGGCTGCTCT | CAAACCTGCTG | GGCTCAAACG | ATCCTCCTGC | 720 |
| CTTGGCCTCC | CAAAGTGCTG | GGGTTACAAG | CATGAACCAT | TATGCCCGGC | CTGCATGCAC | 780 |
| TCTTACACAC | GTTTTATCTG | TTACATATCC | CAAGATGTGT | AGTTCTTTGG | GAAGCAGGAA | 840 |
| GAAATGGGGG | TAACATTGAG | AAGTTAAGGA | AAACTGGTAT | AAATTATTGG | CAGCAGCTCC | 900 |
| TGATTATAGG | TTTTGAGGCC | TGAGTCCATG | GGCAGAGTCC | CTCTCCTGCA | GTTTCATGAGA | 960 |
| TTTGTACCCT | CCAGTGACAG | TACTGGGAAG | GAGGGAATGC | TACGTTCCAA | CTCTTAGTCT | 1020 |
| TCACTTAATT | TTATGACTCA | AAATTCCAGC | TAGATATATA | GGTTACTTTT | ACTGTTGGAT | 1080 |
| CACTCTGGCC | CACGAATGTA | TCCTGCTAAC | TTGATGTGTG | CTCTAACTAC | CTCCTAAGTT | 1140 |
| TGGTGACAGT | CGGCAGAGTT | TGTGAACCAT | GTGATTCCCA | ACTTAAGTTA | CTAACATTTT | 1200 |
| TTTTTTTTTT | TTTTGAGACA | GGATCTTGCT | CTGTCACCCA | GGCTGGAGTG | CAGTGGTACG | 1260 |
| ATCTCAGCTC | ACTGTAGCCT | TAACCCACCC | AGGCTTATGT | GCTCCTCCCA | CCTCAGCCTC | 1320 |
| CCGAGTAGTT | GGAACATATAG | GTGCATACCA | CCATGCCTGG | CTAATTTTTG | TATTTTTTGT | 1380 |
| AGAGGCAGGG | TTTTGCCCTG | TTGCCCAGGC | TGGTCTTGAA | CTCCTGAGCT | CAAGCAATCC | 1440 |
| TCCCACCTCA | GCCTCCCAA | GGGTTGGGAT | TACAGGTGTG | AGCCACTGCA | CCCGGCCAAG | 1500 |
| TTACTAACAT | TTTAAGTCTA | AAGTAAAAGA | TTGCTTCTGT | ATGTTCTCCC | CCAGGTGTGT | 1560 |
| AGGTCCATCC | TGGGAAGGCC | ATCAGACACA | CCTAGTCCAT | GGGTGACACC | CAGCCAGTTT | 1620 |
| TTAATGCCAG | TTCCTCTGGC | AGTTTTTAAT | TTAGGCACTC | GGAAGTGAAA | CCCGGACATT | 1680 |
| CACTGGAAAT | GACTTTAGGA | CAAGACCTGC | TGGCCATGAG | CTGAGAAATG | TCTTACTCTC | 1740 |
| TTGCAGGGAG | AATGCTGTTG | AAAGACTTGA | TTCATTAATA | CAAGCGACTC | ACGTTGCAAT | 1800 |
| GAGAGGCAAC | TCCGATTACG | CTGATCTTAG | TGATGGCTGG | CTCGAAATAA | TACGTGTAGA | 1860 |
| TGCCCCTGAT | CCAGGTGCAG | ACCCGCTGGC | TAGCAGTGTG | AACGGCATGT | GCCTGGATAT | 1920 |
| TCCTGCTCAC | CTGAGCATCC | GCATCCTCAT | CTCGGATGCT | GGCGCGGTGG | AAGGGATTAC | 1980 |
| TCAGCAGGAG | ATACTCGGTG | TAGAGACAAG | GTTCTCCTCA | GTGAACTGGC | AGTACCAGTG | 2040 |
| TGGGCTTACC | TGTGAGCACA | AGGCCGACCT | TCTCCCTATC | AGTGCATCCG | TCCAGTTTAT | 2100 |
| TAAAATTCCCT | GCACAGTTAC | CCCACCCCTT | GACAAGATTC | CAGATCAATT | ATACAGAGTA | 2160 |
| TGACTGCAAC | AGAAATGAGG | TGTGTTGGCC | GCAGCTTCTA | TATCCATGGA | CTCAGTATTA | 2220 |
| TCAAGGGGAG | CTGCATTCTC | AGTGTGTTGC | TAAGGGCTTA | CTGTTGCTGT | TGTTCTCTAC | 2280 |
| ATTGGCCTTG | TTCCTCAGCA | ACCCCTGGAC | CAGAAATATGC | AAAGCCTATA | GTTAGACAAC | 2340 |

CACCTGGCTT TTATTTTTTT GAGATGGAGT TTTGCTCTTG TTACCCAGGC TGGAGTGCAG 2400
 TGCACAATCT CGGCTCACTG CAATCTCTGC CTCCCAAGCA ATCCTCCCAC CTCAGCCTCT 2460
 GGTGTAGCTG GGACCACAGA TGCTCCACCA TGCCTGGCTG TATTTTTTGGT AAAGATGGGG 2520
 TTTCGCCTTG TTGCCCAGGG TGGTCTGTAA CTCCTGAGCT CAGATGATCT GCCCACCTCG 2580
 GCCTCCCAAA GTGCTGGGAT CACAGACGTG AGCCACTGCG TCCGGTCCAT CTGACTTCTC 2640
 AAAGACTTTA GACCTTGACT TCAGTGATTT GTTGTAGTCT TGTATGCTTC TCTATAAAAT 2700
 TTTAATAAAT GAAATGTCTT ATTTTGTAG AAAATTTTAA AAAAAAAAAA AAAA 2754

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met Arg Gly Asn Ser Asp Tyr Ala Asp Leu Ser Asp Gly Trp Leu Glu
 1 5 10 15
 Ile Ile Arg Val Asp Ala Pro Asp Pro Gly Ala Asp Pro Leu Ala Ser
 20 25 30
 Ser Val Asn Gly Met Cys Leu Asp Ile Pro Ala His Leu Ser Ile Arg
 35 40 45
 Ile Leu Ile Ser Asp Ala Gly Ala Val Glu Gly Ile Thr Gln Gln Glu
 50 55 60
 Ile Leu Gly Val Glu Thr Arg Phe Ser Ser Val Asn Trp Gln Tyr Gln
 65 70 75 80
 Cys Gly Leu Thr Cys Glu His Lys Ala Asp Leu Leu Pro Ile Ser Ala
 85 90 95
 Ser Val Gln Phe Ile Lys Ile Pro Ala Gln Leu Pro His Pro Leu Thr
 100 105 110
 Arg Phe Gln Ile Asn Tyr Thr Glu Tyr Asp Cys Asn Arg Asn Glu Val
 115 120 125
 Cys Trp Pro Gln Leu Leu Tyr Pro Trp Thr Gln Tyr Gln Gly Glu
 130 135 140
 Leu His Ser Gln Cys Val Ala Lys Gly Leu Leu Leu Leu Phe Leu

| | | | |
|---|-----|-----|-----|
| 145 | 150 | 155 | 160 |
| Thr Leu Ala Leu Phe Leu Ser Asn Pro Trp Thr Arg Ile Cys Lys Ala | | | |
| | 165 | 170 | 175 |
| Tyr Ser | | | |

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1363 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

| | |
|--|------|
| TAGGCCATGA AGGCCGTTT TTCATAAAAT AGGAATGAGG ACAAATGTTG CTCTTCATCC | 60 |
| TACCAGCTGT TTGTTCTTTG GTAGGGGATC ATGAGTGGAA AAACAAAGGC AAGAAGGGCT | 120 |
| GCCATGTTTTT TTAGACGTTG CTCTGAAGAC GCCAGCGGTA GCGCCAGTGG CAATGCTTTG | 180 |
| TTATCAGAGG ACGAAAATCC TGATGCGAAT GGGGTAACTC GATCATGGAA GATTATTCTA | 240 |
| AGTACAATGC TTACACTGAC TTTTCTTCTT GTAGGACTCC TAAATCATCA GTGGCTTAAA | 300 |
| GAAACAGATG TTCCTCAGAA ATCCAGACAA TTATATGCCA TAATTGCAGA ATATGGTTCA | 360 |
| AGGCTTTTATA AATATCAGGC CAGACTTCGT ATGCCTAAAG AGCAACTGGA ACTTTTAAAG | 420 |
| AAGGAAAGCC AGAATCTGGA AAACAATTTT CGTCAAATTC TATTTTTGAT CGAACAAATA | 480 |
| GATGTCCTGA AGGCATTGCT AAGAGATATG AAGGATGGTA TGGACAATAA TCACAACCTGG | 540 |
| AACACCCATG GAGACCCTGT GGAGGACCCG GACCACACAG AGGAAGTGTC AAACCTTGGTC | 600 |
| AATTATGTAC TTAAAAAGTT GAGAGAAGAC CAAGTCGAGA TGGCTGATTA TGCCCTGAAG | 660 |
| TCGGCCGAG CCTCCATCAT TGAAGCTGGG ACCTCAGAAA GTTATAAAAA TAATAAAGCA | 720 |
| AAATTGTACT GGCATGGGAT AGGTTTCCTA AATCATGAAA TGCCTCCAGA TATTATTCTT | 780 |
| CAGCCGGATG TCTACCCTGG AAAGTGCTGG GCTTTTCCAG GTTCCCAGGG TCATACCCTA | 840 |
| ATCAAGCTTT ACAAAGATCA TACCAACTGC TGTTACCATG GAGCACATCT CAGAGAAGGT | 900 |
| GTCTCCGTCA GGAAACATCT CCAGTGCACC CAAGGAATTT TCTGTCTATG GCATCACAAA | 960 |
| AAAATGTGAA GGAGAAGAAA TTTTCCTAGG TCAGTTTATA TATAACAAAA CAGGAACCAC | 1020 |
| CGTTCAAACA TTTGAACTCC AGCATGCAGT TTCTGAATAT TTATTATGTG TGAAACTTAA | 1080 |

TATCTTTAGC AACTGGGGAC ACCCGAAGTA TACTTGTTTA TATCGATTCA GGGTCCATGG 1140
CACACCAGGC AAGCACATCT AGAAGAGTTG GTACAGAAGG CCATGCCACA TGTCCAGAAT 1200
ATTCAAGAAT GCTTATTCTC TTAGATGATA CCGCACCCAT AGGAATTGAG AATTGGGAGT 1260
GGGAAGAAAA CCTCAAAGTG GTTCATACTT GCCTGTAAAA AGTAAATGCA TTTTACTAAT 1320
AAAAAATAT GGAAGTAAAT TAAAAA AAA 1363

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Gly | Lys | Thr | Lys | Ala | Arg | Arg | Ala | Ala | Met | Phe | Phe | Arg | Arg | 1 | 5 | 10 | 15 |
| Cys | Ser | Glu | Asp | Ala | Ser | Gly | Ser | Ala | Ser | Gly | Asn | Ala | Leu | Leu | Ser | 20 | 25 | 30 | |
| Glu | Asp | Glu | Asn | Pro | Asp | Ala | Asn | Gly | Val | Thr | Arg | Ser | Trp | Lys | Ile | 35 | 40 | 45 | |
| Ile | Leu | Ser | Thr | Met | Leu | Thr | Leu | Thr | Phe | Leu | Leu | Val | Gly | Leu | Leu | 50 | 55 | 60 | |
| Asn | His | Gln | Trp | Leu | Lys | Glu | Thr | Asp | Val | Pro | Gln | Lys | Ser | Arg | Gln | 65 | 70 | 75 | 80 |
| Leu | Tyr | Ala | Ile | Ile | Ala | Glu | Tyr | Gly | Ser | Arg | Leu | Tyr | Lys | Tyr | Gln | 85 | 90 | 95 | |
| Ala | Arg | Leu | Arg | Met | Pro | Lys | Glu | Gln | Leu | Glu | Leu | Leu | Lys | Lys | Glu | 100 | 105 | 110 | |
| Ser | Gln | Asn | Leu | Glu | Asn | Asn | Phe | Arg | Gln | Ile | Leu | Phe | Leu | Ile | Glu | 115 | 120 | 125 | |
| Gln | Ile | Asp | Val | Leu | Lys | Ala | Leu | Leu | Arg | Asp | Met | Lys | Asp | Gly | Met | 130 | 135 | 140 | |
| Asp | Asn | Asn | His | Asn | Trp | Asn | Thr | His | Gly | Asp | Pro | Val | Glu | Asp | Pro | 145 | 150 | 155 | 160 |
| Asp | His | Thr | Glu | Glu | Val | Ser | Asn | Leu | Val | Asn | Tyr | Val | Leu | Lys | Lys | | | | |

| | | | | | |
|---|-----|-----|-----|--|-----|
| | 165 | | 170 | | 175 |
| Leu Arg Glu Asp Gln Val Glu Met Ala Asp Tyr Ala Leu Lys Ser Ala | | | | | |
| | 180 | | 185 | | 190 |
| Gly Ala Ser Ile Ile Glu Ala Gly Thr Ser Glu Ser Tyr Lys Asn Asn | | | | | |
| | 195 | | 200 | | 205 |
| Lys Ala Lys Leu Tyr Trp His Gly Ile Gly Phe Leu Asn His Glu Met | | | | | |
| | 210 | | 215 | | 220 |
| Pro Pro Asp Ile Ile Leu Gln Pro Asp Val Tyr Pro Gly Lys Cys Trp | | | | | |
| | 225 | | 230 | | 240 |
| Ala Phe Pro Gly Ser Gln Gly His Thr Leu Ile Lys Leu Tyr Lys Asp | | | | | |
| | | 245 | 250 | | 255 |
| His Thr Asn Cys Cys Tyr His Gly Ala His Leu Arg Glu Gly Val Ser | | | | | |
| | 260 | | 265 | | 270 |
| Val Arg Lys His Leu Gln Cys Thr Gln Gly Ile Phe Cys Leu Trp His | | | | | |
| | 275 | | 280 | | 285 |
| His Lys Lys Met | | | | | |
| | 290 | | | | |

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2911 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

| | |
|--|-----|
| GGGCTGCATT TCCAGCAGGA GCTGCGAGCA CAGTGCTGGC TCACAACAAG ATGCTCAAGG | 60 |
| TGTCAGCCGT ACTGTGTGTG TGTGCAGCCG CTTGGTGCAG TCAGTCTCTC GCAGCTGCCG | 120 |
| CGGCGGTGGC TGCAGCCGGG GGGCGGTCGG ACGGCGGTAA TTTTCTGGAT GATAACAAT | 180 |
| GGCTCACCAC AATCTCTCAG TATGACAAGG AAGTCGGACA GTGGAACAAA TTCCGAGACG | 240 |
| AAGTAGAGGA TGATTATTTT CGCACTTGGA GTCCAGGAAA ACCCTTCGAT CAGGCTTTAG | 300 |
| ATCCAGCTAA GGATCCATGC TTAAAGATGA AATGTAGTCG CCATAAAGTA TGCATTGCTC | 360 |
| AAGATTCTCA GACTGCAGTC TGCATTAGTC ACCGGAGGCT TACACACAGG ATGAAAGAAG | 420 |
| CAGGAGTAGA CCATAGGCAG TGGAGGGGTC CCATATTATC CACCTGCAAG CAGTGCCCAG | 480 |
| TGGTCTATCC CAGCCCTGTT TGTGGTTCAG ATGGTCATAC CTA CTCTTTT CAGTGCAAAC | 540 |

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|------|
| TAGAATATCA | GGCATGTGTC | TTAGGAAAAC | AGATCTCAGT | CAAATGTGAA | GGACATTGCC | 600 |
| CATGTCCTTC | AGATAAGCCC | ACCAGTACAA | GCAGAAATGT | TAAGAGAGCA | TGCAGTGACC | 660 |
| TGGAGTTCAG | GGAAGTGGCA | AACAGATTGC | GGGACTGGTT | CAAGGCCCTT | CATGAAAAGTG | 720 |
| GAAGTCAAAA | CAAGAAGACA | AAAACATTGC | TGAGGCCTGA | GAGAAGCAGA | TTCGATACCA | 780 |
| GCATCTTGCC | AATTTGCAAG | GACTCACTTG | GCTGGATGTT | TAACAGACTT | GATACAAACT | 840 |
| ATGACCTGCT | ATTGGACCAG | TCAGAGCTCA | GAAGCATTTA | CCTTGATAAG | AATGAACAGT | 900 |
| GTACCAAGGC | ATTCTTCAAT | TCTTGTGACA | CATACAAGGA | CAGTTTAATA | TCTAATAATG | 960 |
| AGTGGTGCTA | CTGCTTCCAG | AGACAGCAAG | ACCCACCTTG | CCAGACTGAG | CTCAGCAATA | 1020 |
| TTCAGAAGCG | GCAAGGGGTT | AAGAAGCTCC | TAGGACAGTA | TATCCCCCTG | TGTGATGAAG | 1080 |
| ATGGTTACTA | CAAGCCAACA | CAATGTCATG | GCAGTGTGTT | ACAGTGCTGG | TGTGTTGACA | 1140 |
| GATATGGAAA | TGAAGTCATG | GGATCCAGAA | TAAATGGTGT | TGCAGATTGT | GCTATAGATT | 1200 |
| TTGAGATCTC | CGGAGATTTT | GCTAGTGGCG | ATTTTCATGA | ATGGACTGAT | GATGAGGATG | 1260 |
| ATGAAGACGA | TATTATGAAT | GATGAAGATG | AAATTGAAGA | TGATGATGAA | GATGAAGGGG | 1320 |
| ATGATGATGA | TGGTGGTGAT | GACCATGATG | TATACATTTA | ATTGATGACA | GTTGAAATCA | 1380 |
| ATAAATTCTA | CATTTCTAAT | ATTTACAAAA | ATGATAGCCT | ATTTAAAAAT | ATCTTCTTCC | 1440 |
| CCAATAACAA | AATGATTCTA | AACCTCACAT | ATATTTTGTA | TAATTATTTG | AAAAAATTGCA | 1500 |
| GCTAAAGTTA | TAGAACTTTA | TGTTTAAATA | AGAATCATTT | GCTTTGAGTT | TTTATATTCC | 1560 |
| TTACACAAAA | AGAAAATACA | TATGCAGTCT | AGTCAGACAA | AATAAAGTTT | TGAAGTGCTA | 1620 |
| CTATAATAAG | TTTTTCACGA | GAACAAACTT | TGTAAATCTT | CCATAAGCAA | AATGACAGCT | 1680 |
| AGTGCTTGGG | ATCGTACATG | TTAATTTTCT | GAAAGATAAT | TCTAAGTGAA | ATTTAAAAATA | 1740 |
| AATAAATTTT | TAATGACCTG | GGTCTTAAGG | ATTTAGGAAA | AATATGCATG | CTTTAATTGC | 1800 |
| ATTTCCAAAG | TAGCATCTTG | CTAGACCTAG | TTGAGTCAGG | ATAACAGAGA | GATACCACAT | 1860 |
| GGCAAGAAAA | ACAAAGTGAC | AATTGTAGAG | TCCTCAATTG | TGTTTACATT | AATAGTGGTG | 1920 |
| TTTTTACCTA | TGAAATTATT | CTGGATCTAA | TAGGACATTT | TACAAAATGG | CAAGTATGGA | 1980 |
| AAACCATGGA | TTCTGAAAGT | TAAAAATTTA | GTTGTTCTCC | CCAATGTGTA | TTTTAATTTG | 2040 |
| GATGGCAGTC | TCATGCAGAT | TTTTTAAAAG | ATCTTTAAT | AACATGATTT | GTTTGCCTTT | 2100 |
| CTAGATTTCT | TTATCTTTCT | GACCAGCAAC | TTAGGGAGCA | GAATTTAAAT | TAGGAAGACA | 2160 |
| AAGGGAAAAGA | TTCATTTAAA | CCATATTTTT | ACAAAGTTTG | TCATTTGCCC | CAAGGTCAAA | 2220 |

TTTAAATTC TTAATTTTCA TTTTATTTC CATTTTAGGT AAAAGTTTGC ATTTAATCTT 2280
 AGAATTATGT TATTTTGTG AGTAGTGTGG AAAGTTAGAG AACTTATTGT ATGGTGCCTT 2340
 GCAAAAATAG AGATAGAAAG ATTTTAGCAT GCATACCAAT ATAGTATATT ACGCAATATA 2400
 TAAGCACACC TAATTAACAG ATTAATATCA GTAAAGGTAT TGCTGCTGGA ATGAAGAAAA 2460
 TGGGATACGT TTGTTTCTTT TTTTCTATTG TWACATAATT GCCATGTGGA CTTGTTTATG 2520
 ATTATTGTGT AGAGTAGCAT TTAAGATTTA ACTGTAGCAA AAATTACTTT AACCGCTGTA 2580
 TTTAAGTTAG CATGTTAATT AATTGTGTAG ACATTTTGGC ACACCATCAC TTTTAACTAT 2640
 ATCATACCAA TGGTTTTGTG CCCATAATAA AAATGGAAAA ACCTGTTGAA TGTTACGTAT 2700
 TGGTATCTTT AATTTCACAA GTGGGTAAAC TGGTTTCCCA GTATACAATT CATTGAAAGC 2760
 AAAATTGATT AATTATTTCC ATTTAATTTA TACACACTCA ATACAAAATT TAATGTTGAC 2820
 TTTACGTAAT AAAGTATAAT GCATTTTCTT TTTTACTGTT TATGTATAGT TTACAAAATA 2880
 AAGAATCTTG TAACCAAAAA AAAAAAAAAA A 2911

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Lys | Val | Ser | Ala | Val | Leu | Cys | Val | Cys | Ala | Ala | Ala | Trp | Cys |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ser | Gln | Ser | Leu | Ala | Ala | Ala | Ala | Ala | Val | Ala | Ala | Ala | Gly | Gly | Arg |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ser | Asp | Gly | Gly | Asn | Phe | Leu | Asp | Asp | Lys | Gln | Trp | Leu | Thr | Thr | Ile |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ser | Gln | Tyr | Asp | Lys | Glu | Val | Gly | Gln | Trp | Asn | Lys | Phe | Arg | Asp | Glu |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Val | Glu | Asp | Asp | Tyr | Phe | Arg | Thr | Trp | Ser | Pro | Gly | Lys | Pro | Phe | Asp |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Gln | Ala | Leu | Asp | Pro | Ala | Lys | Asp | Pro | Cys | Leu | Lys | Met | Lys | Cys | Ser |
| | | | | 85 | | | | | 90 | | | | | 95 | |

Arg His Lys Val Cys Ile Ala Gln Asp Ser Gln Thr Ala Val Cys Ile
100 105 110

Ser His Arg Arg Leu Thr His Arg Met Lys Glu Ala Gly Val Asp His
115 120 125

Arg Gln Trp Arg Gly Pro Ile Leu Ser Thr Cys Lys Gln Cys Pro Val
130 135 140

Val Tyr Pro Ser Pro Val Cys Gly Ser Asp Gly His Thr Tyr Ser Phe
145 150 155 160

Gln Cys Lys Leu Glu Tyr Gln Ala Cys Val Leu Gly Lys Gln Ile Ser
165 170 175

Val Lys Cys Glu Gly His Cys Pro Cys Pro Ser Asp Lys Pro Thr Ser
180 185 190

Thr Ser Arg Asn Val Lys Arg Ala Cys Ser Asp Leu Glu Phe Arg Glu
195 200 205

Val Ala Asn Arg Leu Arg Asp Trp Phe Lys Ala Leu His Glu Ser Gly
210 215 220

Ser Gln Asn Lys Lys Thr Lys Thr Leu Leu Arg Pro Glu Arg Ser Arg
225 230 235 240

Phe Asp Thr Ser Ile Leu Pro Ile Cys Lys Asp Ser Leu Gly Trp Met
245 250 255

Phe Asn Arg Leu Asp Thr Asn Tyr Asp Leu Leu Leu Asp Gln Ser Glu
260 265 270

Leu Arg Ser Ile Tyr Leu Asp Lys Asn Glu Gln Cys Thr Lys Ala Phe
275 280 285

Phe Asn Ser Cys Asp Thr Tyr Lys Asp Ser Leu Ile Ser Asn Asn Glu
290 295 300

Trp Cys Tyr Cys Phe Gln Arg Gln Gln Asp Pro Pro Cys Gln Thr Glu
305 310 315 320

Leu Ser Asn Ile Gln Lys Arg Gln Gly Val Lys Lys Leu Leu Gly Gln
325 330 335

Tyr Ile Pro Leu Cys Asp Glu Asp Gly Tyr Tyr Lys Pro Thr Gln Cys
340 345 350

His Gly Ser Val Gly Gln Cys Trp Cys Val Asp Arg Tyr Gly Asn Glu
355 360 365

Val Met Gly Ser Arg Ile Asn Gly Val Ala Asp Cys Ala Ile Asp Phe
370 375 380

Glu Ile Ser Gly Asp Phe Ala Ser Gly Asp Phe His Glu Trp Thr Asp
385 390 395 400

Asp Glu Asp Asp Glu Asp Asp Ile Met Asn Asp Glu Asp Glu Ile Glu
405 410 415

Asp Asp Asp Glu Asp Glu Gly Asp Asp Asp Asp Gly Gly Asp Asp His
420 425 430

Asp Val Tyr Ile
435

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4130 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

| | |
|--|------|
| GGATTCTGAAG TTTAAGAAAC TGCATTTTAA AGTGCCCAAA GTTTCATTTT CTTCTACCAA | 60 |
| AACTCCTAAA GATAGTTTAG TCCCAGGTGC AAAGTCTAGC ATAGGTCTTT CCACGATTCC | 120 |
| TTTATCATCT TCAGAATGCT CAAGTTTGA ATTACAACAG GTTTCGGCTT GTTCAGAGCC | 180 |
| ATCCATGCAG ATGCCTAAGG TGGGTTTTGC TGGGTTTCCA TCATCCCGGC TTGATCTCAC | 240 |
| TGGTCCTCAC TTTGAATCTT CTATTCTCTC TCCCTGTGAG GATGTTACAC TTACAAAATA | 300 |
| CCAGGTGACT GTTCCCCAGA GCTGCCTTGG CCCCTGAGCT TGCTCTGGAA ATTCCTTCTG | 360 |
| GGTCTCAGGC TGATATTCTT CTTCCCAAGA CAGAGTGCTC CACTGAMCTG CAGCCTCCAG | 420 |
| ARGGAGTTCC AACATCTCAA GCTGAGAGTC ACTCTGGCCC ACTGAATTCC ATGATTCTCTG | 480 |
| TTTCTCTTGG TCAGGTGTCT TTTCTTAAAT TCTATAAACC AAAGTTTGTG TTTTCAGTCC | 540 |
| CCCAAATGGC AGTTCCTGAG GGAGACCTAC ATGCAGCAGT GGGTGCCCCA GTCATGTYTC | 600 |
| YTCTTAGCCC TTGGAGAAAG AGTGCAGTGC CCCTTGCCAA GCACCCAGYT GCCATCCCCA | 660 |
| GGCACCTGTG TGTCCCAGGG CCCAGAAGAG CTTGTGGCCT CCTTGCAGAC ATCAGTAGTG | 720 |
| GCCCYTGGAG AAGCCCCTTC TGAAGATGCT GACCACGAAG GGAAAGGGAG TCCCTTGAAA | 780 |
| ATGCCTAAGA TTAAGCTTCC ATCATTTAGG TGGTCCCCGA AGAAGGAAAC AGGGCCAAAG | 840 |
| GTGGACCCAG AATGCAGCGT GGAGGACTCA AAACCTCAGCC TGGTTTTAGA CAAGGATGAA | 900 |
| GTGGCCCCGC AGTCTGCCAT CCACATGGAT CTGCCCTCTG AGAGGGATGG AGAGAAGGGG | 960 |
| AGGAGCACAA AGCCTGGCTT TGCCATGCCA AAACCTGCAC TTCCCAAAT GAAGGCTTCT | 1020 |

AAGAGTGGGG TCAGCCTGCC ACAGAGAGAC GTGGATCCTT CCCTTTCTAG TGCCACAGCA 1080
GGGGGTAGCT TTCAAGACAC AGAAAAGGCC AGCAGTGACG GTGGTAGGGG AGGACTTGGT 1140
GCAACAGCAA GTGCCACAGG AAGTGAGGGT GTGAACCTCC ACCGGCCACA GGTCCACATT 1200
CCCAGTTTGG GCTTTGCCAA ACCTGATCTC AGATCCTCCA AGGCCAAGGT GGAGGTGAGC 1260
CAGCCTGAAG CTGACCTGCC TCTTCCCAA CATGATCTGT CTACCGAAGG TGACAGCAGA 1320
GGATGTGGGC TCGAGGATGT CCCAGTGAGC CAGCCTTG TG GGGAGGGGAT AGCCCCACA 1380
CCTGAAGATC CCCTCCAGCC ATCCTGTAGA AAACCAGATG CTGAAGTCCT CACAGTGGA 1440
AGCCCAGAGG AGGAAGCCAT GACCAAGGAC TCGCAGGAAA GCTGGTTTAA AATGCCCAAG 1500
TTCCGCATGC CCAGCCTTAG GCGCTCTTTC AGGGACAGAG GCGGGGCTGG AAAGCTGGAA 1560
GTGGCTCAGA CACAGGCACC GGCAGCAACA GGGGGTGAAG CAGCAGCTAA AGTCAAAGAG 1620
TTCCTTGTTT CTGGGTCAAA CGTGAGGCA GCTATGTCCC TACAGCTCCC AGAGGCAGAT 1680
GCAGAAGTGA CAGCTTCTGA GAGCAAATCA TCCACAGATA TTCTAAGGTG TGATCTTGAC 1740
AGCACAGGCT TGAAGCTGCA CCTTTCCACT GCTGGGATGA CTGGGGATGA GCTTTCCACT 1800
TCTGAGGTCA GGATCCATCC ATCCAAAGGA CCTCTCCCTT TTCAGATGCC TGGCATGAGG 1860
CTTCCAGAAA CCCAGGTTCT TCCAGGAGAA ATAGATGAGA CTCCTCTTTC CAAGCCAGGA 1920
CATGACCTTG CCAGCATGGA GGATAAAACA GAGAAATGGT CTTCCCAGCC TGAAGGTCCA 1980
CTTAAATTGA AAGCTTCAAG TACTGATATG CCATCCCAGA TTTCTGTGGT TAATGTGGAT 2040
CAACTGTGGG AAGATTCTGT CCTAACTGTC AAATTCCCCA AATTAATGGT ACCAAGGTTC 2100
TCCTTCGCTG CCCCAGCTC AGAGGATGAT GTGTTTCATCC CCACTGTGAG GGAAGTGCAG 2160
TGTCAGAGG CCAATATTGA TACAGCCCTT TGTAAGGAAA GTCCGGGGCT CTGGGGAGCC 2220
AGCATCCTGA AGGCAGGTGC TGGGGTCCCT GGGGAGCAGC CTGTGGACCT TAACCTGCCT 2280
TTGGAAGCTC CCCCAATTTC AAAGGTCAGA GTGCATATTC AGGGTGCTCA GGTGAAAAGT 2340
CAAGAGGTCA CTATACACAG CATAGTGACA CCAGAGTTTG TAGATCTCTC AGTACCCAGG 2400
ACTTTTCCA CTCAGATTGT GCGGGAATCA GAGATCCCCA CGTCAGAGAT TCAAACACCT 2460
TCGTACGGAT TTTCCTTATT AAAAGTGAAA ATCCCAGAGC CCCACACGCA GGCTAGAGTG 2520
TACACAACAA TGACTCAACA CTCTAGGACT CAGGAGGGCA CAGAAGAGGC TCCCATACAA 2580
GCCACCCAG GAGTAGACTC CATTTCTGGA GATCTCCAGC CTGACACTGG AGAACCATT 2640
GAGATGATCT CTTCCAGCGT CAATGTACTG GGACAGCAAA CACTCACATT TGAAGTTCCT 2700

| | |
|--|------|
| TCTGGCCACC AGCTTGCAGA CAGCTGTTCA GATGAGGAGC CAGCAGAAAT TCTTGAGTTT | 2760 |
| CCCCCTGATG ATAGCCAAGA GGCAACCACA CCACTGGCAG ATGAAGGCAG GGCTCCAAAA | 2820 |
| GACAAACCAG AAAGTAAAAA ATCTGGTCTG CTCTGGTTTTT GGCTTCCAAA CATTGGGTTT | 2880 |
| TCCTCTTCTG TTGATGAGAC AGGTGTTGAT TCCAAAAATG ACGTCCAGAG ATCTGCTCCC | 2940 |
| ATTCAAACAC AGCCTGAGGC ACGACCAGAG GCAGAACTGC CTAAAAAACA GGAGAAGGCA | 3000 |
| GGCTGGTTCC GATTTCCCAA ATTAGGGTTC TCCTCATCTC CTACCAAGAA AAGCAAAAGC | 3060 |
| ACCGAAGATG GGGCAGAGCT GGAAGAACAA AAACCTCAAG AAGAAACAAT CACGTTTTTC | 3120 |
| GATGCCCCGAG AAAGTTTCTC CCCTGAAGAG AAGGAAGAGG GTGAACTGAT CGGGCCTGTG | 3180 |
| GGCACTGGGC TGGACTCCAG AGTGATGGTG ACATCCGCGG CAAGAACAGA GTTAATCCTG | 3240 |
| CCCGAGCAGG ACAGAAAAGC TGACGATGAA AGCAAAGGGT CAGGCCTGGG ACCAAATGAA | 3300 |
| GGCTGAGAGG TATGGCTCAT CGGTACAAGA GAGATGCAAA AAATAAGTT GGAAAGTAAA | 3360 |
| GGCTACACAC ACATATGGAG CACCCCATCC CACAGCACAT TACATCCACC TCACTTCACA | 3420 |
| GAACGGAGAA CAGAGCAGAA ATGACCAGAA CACCTTTGTC ACCATCACAC AGCCCTCCTA | 3480 |
| AAATGGAACC AAAGCTTCCC AGCTCCCTCA AAGCTTTGGA TGCAAAGAAG GCACCCTGAC | 3540 |
| TTCCACAAGA CACCAGAATT CACACGGTAC TCAGAGGCAC TGCTGGGGAA GTTTGTTGGT | 3600 |
| CTTTATTAGA TAAATTTCCTA GAGACCTGTC CATAATACCC AACAGAACAT GACTGTTTCT | 3660 |
| TTGAGGAAAAG GGTATAATG TCTGTGGTGT ACAAGTCGTT TTTGGTATAA CTTCTTTCCT | 3720 |
| GCTGCTGCTG CTTCCCGGCA AACATAGTTT TCCTATTTCA GGCAGAGTGC GGTATATTCC | 3780 |
| AGGAAACACT GTTTCCTACT CACTTAGCTT ACTTCTTTGT TGAATGCCTC ACTAATGGCA | 3840 |
| AGTTTCAAGA TGTTTTGGGT GACAATGCAC ACATGCTGGG CAAAAGGGTG ATGGCCAGTG | 3900 |
| GCTGGCAGCT GGGCCAGCAG AAGCTAGGAC ATCTGTGAGT TGTCATTCTC ATCTATCCAT | 3960 |
| GTCCACTGGC CTGCCAGCAT CCGCCAGTGC CTTGCCAGTG TGCACGGTCC CACACTGTGG | 4020 |
| CCCCTGAGTC CCCTAATGTA CACGCTGCAG CCAGAATGCA GATGGAGCTG GCTTGGCTGT | 4080 |
| TCCCTGGATG GGCAATAAAG AAAGTGCTGC ATCCCCAAAAA AAAAAAAAAA | 4130 |

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 911 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Gln | Trp | Val | Pro | Gln | Ser | Cys | Xaa | Xaa | Leu | Ala | Leu | Gly | Glu | 1 | 5 | 10 | 15 |
| Arg | Val | Gln | Cys | Pro | Leu | Pro | Ser | Thr | Gln | Leu | Pro | Ser | Pro | Gly | Thr | 20 | 25 | 30 | |
| Cys | Val | Ser | Gln | Gly | Pro | Glu | Glu | Leu | Val | Ala | Ser | Leu | Gln | Thr | Ser | 35 | 40 | 45 | |
| Val | Val | Ala | Xaa | Gly | Glu | Ala | Pro | Ser | Glu | Asp | Ala | Asp | His | Glu | Gly | 50 | 55 | 60 | |
| Lys | Gly | Ser | Pro | Leu | Lys | Met | Pro | Lys | Ile | Lys | Leu | Pro | Ser | Phe | Arg | 65 | 70 | 75 | 80 |
| Trp | Ser | Pro | Lys | Lys | Glu | Thr | Gly | Pro | Lys | Val | Asp | Pro | Glu | Cys | Ser | 85 | 90 | 95 | |
| Val | Glu | Asp | Ser | Lys | Leu | Ser | Leu | Val | Leu | Asp | Lys | Asp | Glu | Val | Ala | 100 | 105 | 110 | |
| Pro | Gln | Ser | Ala | Ile | His | Met | Asp | Leu | Pro | Pro | Glu | Arg | Asp | Gly | Glu | 115 | 120 | 125 | |
| Lys | Gly | Arg | Ser | Thr | Lys | Pro | Gly | Phe | Ala | Met | Pro | Lys | Leu | Ala | Leu | 130 | 135 | 140 | |
| Pro | Lys | Met | Lys | Ala | Ser | Lys | Ser | Gly | Val | Ser | Leu | Pro | Gln | Arg | Asp | 145 | 150 | 155 | 160 |
| Val | Asp | Pro | Ser | Leu | Ser | Ser | Ala | Thr | Ala | Gly | Gly | Ser | Phe | Gln | Asp | 165 | 170 | 175 | |
| Thr | Glu | Lys | Ala | Ser | Ser | Asp | Gly | Gly | Arg | Gly | Gly | Leu | Gly | Ala | Thr | 180 | 185 | 190 | |
| Ala | Ser | Ala | Thr | Gly | Ser | Glu | Gly | Val | Asn | Leu | His | Arg | Pro | Gln | Val | 195 | 200 | 205 | |
| His | Ile | Pro | Ser | Leu | Gly | Phe | Ala | Lys | Pro | Asp | Leu | Arg | Ser | Ser | Lys | 210 | 215 | 220 | |
| Ala | Lys | Val | Glu | Val | Ser | Gln | Pro | Glu | Ala | Asp | Leu | Pro | Leu | Pro | Lys | 225 | 230 | 235 | 240 |
| His | Asp | Leu | Ser | Thr | Glu | Gly | Asp | Ser | Arg | Gly | Cys | Gly | Leu | Glu | Asp | 245 | 250 | 255 | |
| Val | Pro | Val | Ser | Gln | Pro | Cys | Gly | Glu | Gly | Ile | Ala | Pro | Thr | Pro | Glu | 260 | 265 | 270 | |

Asp Pro Leu Gln Pro Ser Cys Arg Lys Pro Asp Ala Glu Val Leu Thr
 275 280 285
 Val Glu Ser Pro Glu Glu Glu Ala Met Thr Lys Asp Ser Gln Glu Ser
 290 295 300
 Trp Phe Lys Met Pro Lys Phe Arg Met Pro Ser Leu Arg Arg Ser Phe
 305 310 315 320
 Arg Asp Arg Gly Gly Ala Gly Lys Leu Glu Val Ala Gln Thr Gln Ala
 325 330 335
 Pro Ala Ala Thr Gly Gly Glu Ala Ala Ala Lys Val Lys Glu Phe Leu
 340 345 350
 Val Ser Gly Ser Asn Val Glu Ala Ala Met Ser Leu Gln Leu Pro Glu
 355 360 365
 Ala Asp Ala Glu Val Thr Ala Ser Glu Ser Lys Ser Ser Thr Asp Ile
 370 375 380
 Leu Arg Cys Asp Leu Asp Ser Thr Gly Leu Lys Leu His Leu Ser Thr
 385 390 395 400
 Ala Gly Met Thr Gly Asp Glu Leu Ser Thr Ser Glu Val Arg Ile His
 405 410 415
 Pro Ser Lys Gly Pro Leu Pro Phe Gln Met Pro Gly Met Arg Leu Pro
 420 425 430
 Glu Thr Gln Val Leu Pro Gly Glu Ile Asp Glu Thr Pro Leu Ser Lys
 435 440 445
 Pro Gly His Asp Leu Ala Ser Met Glu Asp Lys Thr Glu Lys Trp Ser
 450 455 460
 Ser Gln Pro Glu Gly Pro Leu Lys Leu Lys Ala Ser Ser Thr Asp Met
 465 470 475 480
 Pro Ser Gln Ile Ser Val Val Asn Val Asp Gln Leu Trp Glu Asp Ser
 485 490 495
 Val Leu Thr Val Lys Phe Pro Lys Leu Met Val Pro Arg Phe Ser Phe
 500 505 510
 Ala Ala Pro Ser Ser Glu Asp Asp Val Phe Ile Pro Thr Val Arg Glu
 515 520 525
 Val Gln Cys Pro Glu Ala Asn Ile Asp Thr Ala Leu Cys Lys Glu Ser
 530 535 540
 Pro Gly Leu Trp Gly Ala Ser Ile Leu Lys Ala Gly Ala Gly Val Pro
 545 550 555 560
 Gly Glu Gln Pro Val Asp Leu Asn Leu Pro Leu Glu Ala Pro Pro Ile
 565 570 575

Ser Lys Val Arg Val His Ile Gln Gly Ala Gln Val Glu Ser Gln Glu
580 585 590

Val Thr Ile His Ser Ile Val Thr Pro Glu Phe Val Asp Leu Ser Val
595 600 605

Pro Arg Thr Phe Ser Thr Gln Ile Val Arg Glu Ser Glu Ile Pro Thr
610 615 620

Ser Glu Ile Gln Thr Pro Ser Tyr Gly Phe Ser Leu Leu Lys Val Lys
625 630 635 640

Ile Pro Glu Pro His Thr Gln Ala Arg Val Tyr Thr Thr Met Thr Gln
645 650 655

His Ser Arg Thr Gln Glu Gly Thr Glu Glu Ala Pro Ile Gln Ala Thr
660 665 670

Pro Gly Val Asp Ser Ile Ser Gly Asp Leu Gln Pro Asp Thr Gly Glu
675 680 685

Pro Phe Glu Met Ile Ser Ser Ser Val Asn Val Leu Gly Gln Gln Thr
690 695 700

Leu Thr Phe Glu Val Pro Ser Gly His Gln Leu Ala Asp Ser Cys Ser
705 710 715 720

Asp Glu Glu Pro Ala Glu Ile Leu Glu Phe Pro Pro Asp Asp Ser Gln
725 730 735

Glu Ala Thr Thr Pro Leu Ala Asp Glu Gly Arg Ala Pro Lys Asp Lys
740 745 750

Pro Glu Ser Lys Lys Ser Gly Leu Leu Trp Phe Trp Leu Pro Asn Ile
755 760 765

Gly Phe Ser Ser Ser Val Asp Glu Thr Gly Val Asp Ser Lys Asn Asp
770 775 780

Val Gln Arg Ser Ala Pro Ile Gln Thr Gln Pro Glu Ala Arg Pro Glu
785 790 795 800

Ala Glu Leu Pro Lys Lys Gln Glu Lys Ala Gly Trp Phe Arg Phe Pro
805 810 815

Lys Leu Gly Phe Ser Ser Ser Pro Thr Lys Lys Ser Lys Ser Thr Glu
820 825 830

Asp Gly Ala Glu Leu Glu Glu Gln Lys Leu Gln Glu Glu Thr Ile Thr
835 840 845

Phe Phe Asp Ala Arg Glu Ser Phe Ser Pro Glu Glu Lys Glu Glu Gly
850 855 860

Glu Leu Ile Gly Pro Val Gly Thr Gly Leu Asp Ser Arg Val Met Val
865 870 875 880

Thr Ser Ala Ala Arg Thr Glu Leu Ile Leu Pro Glu Gln Asp Arg Lys
885 890 895

Ala Asp Asp Glu Ser Lys Gly Ser Gly Leu Gly Pro Asn Glu Gly
900 905 910

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

| | | | | | | |
|------------|------------|-------------|------------|-------------|------------|------|
| GCTCGTCTCG | CCGGGCTGTT | CGCGGGCAGG | CCCTGCCCTG | AAGGGACGAA | TCGGCTTGGA | 60 |
| GCGCGGGAGG | TGGAGTCGGC | CCCGGCGGTC | GCTCCCTGGA | CCCAACCCGA | GGCTGACCCA | 120 |
| KGCCCCTGCC | CATGCGGGGC | GCCCCCTGGCT | CGGAAGAGTC | CCCCGGGGCCG | GGAGCAGCTC | 180 |
| CAGGCAGCGG | CCCCGGAGGA | AGAGGAAGAA | GGGACAGTGC | TCAGCTTGGG | GGACCCGGAC | 240 |
| CCTCGCCGCG | GCATTTGGAG | CCGGGGGCAG | TCCCGAACTC | TGTGCTTGGC | ACCGCCGCTC | 300 |
| CGAGTAGGGC | AGCGCCTGCC | GGGACTCTGA | CCCGGACCCC | CTGCGCCTCG | TAGGCGGCGG | 360 |
| CGCCGCCGCG | CCACCCTGTT | CTTCCGTGTC | TCCCTCTGCC | TGGCGGCAGT | CACGGCCAAG | 420 |
| AGAGTATTAT | GAGGGAGGCC | GAGGACTTCA | TGCTCCGGAC | AGAGAAACGG | CGCTGGGATT | 480 |
| AGGGATTGCC | ACTTCTGAGA | GGATGCTGGG | AATCTGCAGG | GGGAGACGGA | AATTCTTGGC | 540 |
| TGCCTCGTTG | AGTCTTCTCT | GCATCCCAGC | CATCACCTGG | ATTTACCTGT | TTTCTGGGAG | 600 |
| CTTCGAAGAT | GGAAAGCCCG | TGTCTCTGTC | ACCGCTGGAG | TCCCAGGCAC | ACAGCCCCAG | 660 |
| GTACACGGCC | TCCAGCCAGC | GGGAGCGCGA | GAGCCTGGAG | GTGCGCATGC | GCGAGGTGGA | 720 |
| GGAGGAGAAC | CGCGCCCTCC | GCAGGCAGCT | CAGCCTGGCC | CAGGGCCGAG | CCCCATCCCA | 780 |
| TCGCCGAGGC | AACCACTCCA | AGACCTACTC | CATGGAGGAG | GGCACTGGAG | ACAGCGAGAA | 840 |
| CCTTCGGGCT | GGCATCGTGG | CAGGCAACAG | CTCCGAGTGT | GGGCAGCAGC | CGGTCTGTGA | 900 |
| GAAATGCGAG | ACAATCCACG | TTGCTATTGT | CTGCGCCGGA | TACAATGCCA | GCCGGGATGT | 960 |
| CGTCACCCTG | GTCAAATCCG | TCCTGTTCCA | TAGACGGAAC | CCTCTGCACT | TCCACCTTAT | 1020 |
| TGCTGACTCC | ATTGCGGAGC | AGATCCTGGC | CACGCTCTTC | CAGACCTGGA | TGGTGCCCGC | 1080 |

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|------|
| TGTGCGTGTG | GACTTCTACA | ATGCAGACGA | GCTCAAGTCT | GAAGTTTCCT | GGATCCCCAA | 1140 |
| TAAACATTAC | TCTGGGATTT | ATGGTCTGAT | GAAGCTTGTC | CTGACCAAGA | CTCTTCCTGC | 1200 |
| CAACCTGGAG | AGAGTCATCG | TCCTTGACAC | GGATATCACC | TTTGCCACTG | ACATTGCAGA | 1260 |
| GCTGTGGGCT | GTGTTCCACA | AGTTCAAAGG | TCAGCAAGTC | CTGGGCTTGG | TGGAGAACCA | 1320 |
| GAGTGACTGG | TACCTTGGAA | ACCTGTGGAA | AAATCACCGC | CCATGGCCAG | CCCTTGGAAAG | 1380 |
| AGGCTACAAC | ACAGGGGTGA | TCCTGTTACT | TCTGGATAAG | CTGCGGAAGA | TGAAATGGGA | 1440 |
| GCAGATGTGG | AGGCTGACCG | CAGAGAGGGA | GCTCATGGGC | ATGCTCTCTA | CATCCTTAGC | 1500 |
| TGACCAGGAT | ATTTTCAATG | CCGTCATCAA | ACAAAACCCC | TTCTTTGTGT | ACCAGCTCCC | 1560 |
| CTGCTTCTGG | AATGTGCAGC | TGTCAGACCA | CACCCGCTCC | GAGCAGTGCT | ACAGAGACGT | 1620 |
| GTCTGATCTA | AAGGTCATTC | ACTGGAAGTC | CCCCAAGAAG | CTCCGGGTGA | AGAACAAGCA | 1680 |
| TGTGGAGTTT | TTTCGCAACC | TCTACCTGAC | CTTCCTGGAG | TATGACGGCA | ATCTTCTGAG | 1740 |
| GCGGGAAC TG | TTTGGCTGCC | CCAGTGAGGC | TGATGTCAAC | AGTGAAAACC | TCCAGAAGCA | 1800 |
| GCTGTCTGAG | CTGGACGAGG | ACGACCTGTG | CTATGAGTTC | CGGCGAGAGC | GCTTCACTGT | 1860 |
| CCACCGCACC | CACCTGTACT | TCCTGCACTA | CGAGTATGAG | CCTGCAGCAG | ACAGCACGGA | 1920 |
| CGTCACCTTG | GTGCTCAGC | TGTCCATGGA | CAGGCTCCAG | ATGCTGGAGG | CCATCTGCAA | 1980 |
| GCACTGGGAG | GGGCCCATCA | GCCTGGCCCT | CTACCTGTCA | GACGCCGAGG | CCCAGCAGTT | 2040 |
| CCTCCGCTAC | GCACAGGGCT | CTGAGGTGCT | TATGAGCCGC | CACAACGTGG | GCTACCACAT | 2100 |
| CGTGTAACAAG | GAGGGCCAGT | TCTACCCCGT | GAACCTGCTG | CGCAACGTGG | CCATGAAGCA | 2160 |
| CATCAGCACT | CCCTACATGT | TCCTGTCTGA | CATTGACTTC | CTGCCCATGT | ATGGGCTCTA | 2220 |
| TGAGTACCTC | AGGAAGTCTG | TCATCCAGCT | CGATCTTGCC | AACACCAAGA | AAGCAATGAT | 2280 |
| TGTCCCCGCG | TTGAGACAC | TGCGCTACCG | GCTGTCCCTC | CCCAAGTCAA | AAGCGGAGTT | 2340 |
| GCTGTCAATG | CTGGACATGG | GGACCCCTCT | CACATTGAGG | TACCACGTCT | GGACGAAAGG | 2400 |
| CCACGCACCC | ACAACTTCG | CCAAGTGGCG | GACCGCCACC | ACGCCTTACC | GGGTTGAGTG | 2460 |
| GGAGGCCGAT | TTTGAGCCGT | ATGTTGTTGT | GAGACGTGAC | TGCCCCGAGT | ACGACCGGAG | 2520 |
| GTTTGTAGGC | TTTGGCTGGA | ACAAAGTGGC | TCATATCATG | GAGCTGGATG | TGCAGGAGTA | 2580 |
| TGAGTTCATT | GTGCTGCCCA | ACGCCTACAT | GATCCACATG | CCTCATGCCC | CCAGCTTCGA | 2640 |
| CATTACCAAG | TTCCGTTCGA | ACAAGCAATA | CCGCATCTGT | CTCAAAACCC | TCAAGGAAGA | 2700 |
| GTTTCAGCAG | GACATGTCCC | GCCGCTACGG | CTTTGCTGCC | CTGAAATATC | TCACAGCCGA | 2760 |
| GAACAACAGC | TAGCACCAAG | AAGCCCACCA | CTAGGGGGAG | ACATGCTGTA | GGGGAAGTGC | 2820 |

| | |
|--|------|
| CACTCGCTGT TTGGGGCCCG GCCTTCAAAT TCAAAATTGA GCCATGCTTT TTCGGTTTGT | 2880 |
| TTTTATTTAT CTCTTTGGCC CAGCCAAGCT GCCCTCACTA CAGAGACCTT GGACAAGGAT | 2940 |
| CCAGCCAGTC CCTCTCTGCC CCACAACCCT GCATTCCCAG AGGTTAGCTA TGCAGCCCAC | 3000 |
| CTAGATGAGT CTCTTCAAGA ATGGGAAATC AAGGGGTGAC AGGGAGTAAA AGGGTTATCA | 3060 |
| TCTTACTGCA AAGCCACAAG ATCAGGGCAG GGCTTTAGGA TGTTCCTGGAT GCTTTTTAAT | 3120 |
| AATTATGCTT CCCATCATAA CTGGGGAGAA AGGGAAGTCA GGGTCTAGG GGTATTTCGT | 3180 |
| CCCAGGAAAT AGAAGTGAAA TTGTCTTTAT TAAGTGAAAA CTTTCCCCTT TGCCCTGCAA | 3240 |
| TGTAGCTGGG CATTCAAACG GAGGGCAAAC CGATGATCTA AACCAACCAC TTGGAAAAAC | 3300 |
| CCAATGGGGA CATTGTAACC AGAGGGTCCT GGAGGTGGGG TTGATGGGTT TCCTTATCCC | 3360 |
| CAAAGTCACT CCTGTTTTGT TTTGTTTTTC TTTGGGGGTT TTGTTTATTT TTGGGGCTGG | 3420 |
| CAATCCAAAA TAGAAAACTT GATCCTTTGA GGCTCTAAAG GAAAATCAGC TGCCTCTACC | 3480 |
| AACCACCCCTC TATCAGCAGT GGCCCAAGAA GGAGGTCAAG CATCTTCGGC CGATATTTAA | 3540 |
| ACATGGGCAG CTTCTTCAG GATGATCACC GAGGCTCCCG TGACTTTGAA CTCCTACTC | 3600 |
| TCCAGAATCC AGGGGCTATA GCGATGGGGA CTGCGGAATT ACGAGGGCTG GCTGTTTTAC | 3660 |
| ACCGGTCACA TTTTCTATTG GCAGTGACTG ATTCATGGGA AAGGGCTTTG AAGGAACTAC | 3720 |
| TTCAGTGCAC ACACAAGGTA CGAACCTYTC AGGCCTTTCG AAGAACTTTC ATAATTCATG | 3780 |
| AAAGCCCAGT TYTGAAGATT CACGTATCCA TYTGGAGACC TACAGGAAGA AAGTGATTGG | 3840 |
| GTTCCTCTGG TTCTTGCCCTG CTTCACGTG GATGGGAAGA GGTGACAACC TCAGTCTCCC | 3900 |
| TTTGGGACCT GTCCAAGGGT AGGCAACCAC CTTCACCTTC ACACAGATTG AGGAGACACT | 3960 |
| GGACTTTTTTA CCCATTTTCT TTAATYTTCA ATATTAATAT TGTGTTTACA TTGATGAGAA | 4020 |
| CAAGAGTTAA TGCCCTACCC TCTGCTGGGC TGTGTGTATT GAGTTGCAAT GTGACCAGCG | 4080 |
| AAAGCTGCAT TTAATAAATG AAAGTACAGA CTGAAAAAAA AAAAAAAAAA AAAAAAAAAA | 4140 |
| AA | 4142 |

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gly | Ile | Cys | Arg | Gly | Arg | Arg | Lys | Phe | Leu | Ala | Ala | Ser | Leu | 1 | 5 | 10 | 15 |
| Ser | Leu | Leu | Cys | Ile | Pro | Ala | Ile | Thr | Trp | Ile | Tyr | Leu | Phe | Ser | Gly | 20 | 25 | 30 | |
| Ser | Phe | Glu | Asp | Gly | Lys | Pro | Val | Ser | Leu | Ser | Pro | Leu | Glu | Ser | Gln | 35 | 40 | 45 | |
| Ala | His | Ser | Pro | Arg | Tyr | Thr | Ala | Ser | Ser | Gln | Arg | Glu | Arg | Glu | Ser | 50 | 55 | 60 | |
| Leu | Glu | Val | Arg | Met | Arg | Glu | Val | Glu | Glu | Glu | Asn | Arg | Ala | Leu | Arg | 65 | 70 | 75 | 80 |
| Arg | Gln | Leu | Ser | Leu | Ala | Gln | Gly | Arg | Ala | Pro | Ser | His | Arg | Arg | Gly | 85 | 90 | 95 | |
| Asn | His | Ser | Lys | Thr | Tyr | Ser | Met | Glu | Glu | Gly | Thr | Gly | Asp | Ser | Glu | 100 | 105 | 110 | |
| Asn | Leu | Arg | Ala | Gly | Ile | Val | Ala | Gly | Asn | Ser | Ser | Glu | Cys | Gly | Gln | 115 | 120 | 125 | |
| Gln | Pro | Val | Val | Glu | Lys | Cys | Glu | Thr | Ile | His | Val | Ala | Ile | Val | Cys | 130 | 135 | 140 | |
| Ala | Gly | Tyr | Asn | Ala | Ser | Arg | Asp | Val | Val | Thr | Leu | Val | Lys | Ser | Val | 145 | 150 | 155 | 160 |
| Leu | Phe | His | Arg | Arg | Asn | Pro | Leu | His | Phe | His | Leu | Ile | Ala | Asp | Ser | 165 | 170 | 175 | |
| Ile | Ala | Glu | Gln | Ile | Leu | Ala | Thr | Leu | Phe | Gln | Thr | Trp | Met | Val | Pro | 180 | 185 | 190 | |
| Ala | Val | Arg | Val | Asp | Phe | Tyr | Asn | Ala | Asp | Glu | Leu | Lys | Ser | Glu | Val | 195 | 200 | 205 | |
| Ser | Trp | Ile | Pro | Asn | Lys | His | Tyr | Ser | Gly | Ile | Tyr | Gly | Leu | Met | Lys | 210 | 215 | 220 | |
| Leu | Val | Leu | Thr | Lys | Thr | Leu | Pro | Ala | Asn | Leu | Glu | Arg | Val | Ile | Val | 225 | 230 | 235 | 240 |
| Leu | Asp | Thr | Asp | Ile | Thr | Phe | Ala | Thr | Asp | Ile | Ala | Glu | Leu | Trp | Ala | 245 | 250 | 255 | |
| Val | Phe | His | Lys | Phe | Lys | Gly | Gln | Gln | Val | Leu | Gly | Leu | Val | Glu | Asn | 260 | 265 | 270 | |
| Gln | Ser | Asp | Trp | Tyr | Leu | Gly | Asn | Leu | Trp | Lys | Asn | His | Arg | Pro | Trp | | | | |

| 275 | 280 | 285 |
|--|-----|---------|
| Pro Ala Leu Gly Arg Gly Tyr Asn Thr Gly Val Ile Leu Leu Leu Leu 290 | 295 | 300 |
| Asp Lys Leu Arg Lys Met Lys Trp Glu Gln Met Trp Arg Leu Thr Ala 305 | 310 | 315 320 |
| Glu Arg Glu Leu Met Gly Met Leu Ser Thr Ser Leu Ala Asp Gln Asp 325 | 330 | 335 |
| Ile Phe Asn Ala Val Ile Lys Gln Asn Pro Phe Leu Val Tyr Gln Leu 340 | 345 | 350 |
| Pro Cys Phe Trp Asn Val Gln Leu Ser Asp His Thr Arg Ser Glu Gln 355 | 360 | 365 |
| Cys Tyr Arg Asp Val Ser Asp Leu Lys Val Ile His Trp Asn Ser Pro 370 | 375 | 380 |
| Lys Lys Leu Arg Val Lys Asn Lys His Val Glu Phe Phe Arg Asn Leu 385 | 390 | 395 400 |
| Tyr Leu Thr Phe Leu Glu Tyr Asp Gly Asn Leu Leu Arg Arg Glu Leu 405 | 410 | 415 |
| Phe Gly Cys Pro Ser Glu Ala Asp Val Asn Ser Glu Asn Leu Gln Lys 420 | 425 | 430 |
| Gln Leu Ser Glu Leu Asp Glu Asp Asp Leu Cys Tyr Glu Phe Arg Arg 435 | 440 | 445 |
| Glu Arg Phe Thr Val His Arg Thr His Leu Tyr Phe Leu His Tyr Glu 450 | 455 | 460 |
| Tyr Glu Pro Ala Ala Asp Ser Thr Asp Val Thr Leu Val Ala Gln Leu 465 | 470 | 475 480 |
| Ser Met Asp Arg Leu Gln Met Leu Glu Ala Ile Cys Lys His Trp Glu 485 | 490 | 495 |
| Gly Pro Ile Ser Leu Ala Leu Tyr Leu Ser Asp Ala Glu Ala Gln Gln 500 | 505 | 510 |
| Phe Leu Arg Tyr Ala Gln Gly Ser Glu Val Leu Met Ser Arg His Asn 515 | 520 | 525 |
| Val Gly Tyr His Ile Val Tyr Lys Glu Gly Gln Phe Tyr Pro Val Asn 530 | 535 | 540 |
| Leu Leu Arg Asn Val Ala Met Lys His Ile Ser Thr Pro Tyr Met Phe 545 | 550 | 555 560 |
| Leu Ser Asp Ile Asp Phe Leu Pro Met Tyr Gly Leu Tyr Glu Tyr Leu 565 | 570 | 575 |
| Arg Lys Ser Val Ile Gln Leu Asp Leu Ala Asn Thr Lys Lys Ala Met | | |

| | | |
|---|-------------------------------------|-----|
| 580 | 585 | 590 |
| Ile Val Pro Ala Phe Glu Thr | Leu Arg Tyr Arg Leu Ser Phe Pro Lys | |
| 595 | 600 | 605 |
| Ser Lys Ala Glu Leu Leu Ser Met Leu Asp Met Gly Thr Leu Phe Thr | | |
| 610 | 615 | 620 |
| Phe Arg Tyr His Val Trp Thr Lys Gly His Ala Pro Thr Asn Phe Ala | | |
| 625 | 630 | 635 |
| Lys Trp Arg Thr Ala Thr Thr Pro Tyr Arg Val Glu Trp Glu Ala Asp | | |
| 645 | 650 | 655 |
| Phe Glu Pro Tyr Val Val Val Arg Arg Asp Cys Pro Glu Tyr Asp Arg | | |
| 660 | 665 | 670 |
| Arg Phe Val Gly Phe Gly Trp Asn Lys Val Ala His Ile Met Glu Leu | | |
| 675 | 680 | 685 |
| Asp Val Gln Glu Tyr Glu Phe Ile Val Leu Pro Asn Ala Tyr Met Ile | | |
| 690 | 695 | 700 |
| His Met Pro His Ala Pro Ser Phe Asp Ile Thr Lys Phe Arg Ser Asn | | |
| 705 | 710 | 715 |
| Lys Gln Tyr Arg Ile Cys Leu Lys Thr Leu Lys Glu Glu Phe Gln Gln | | |
| 725 | 730 | 735 |
| Asp Met Ser Arg Arg Tyr Gly Phe Ala Ala Leu Lys Tyr Leu Thr Ala | | |
| 740 | 745 | 750 |
| Glu Asn Asn Ser | | |
| 755 | | |

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1435 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

| | |
|---|-----|
| TGCACCGGTG GTCGGCTGTT GGGTGTGGAG TTTCCAGCG CCCCTCGGGT CCGACCCCTTT | 60 |
| GAGCGTTCTG CTCCGGCGCC AGCCTACCTC GCTCCTCGGC GCCATGACCA CAACCACCAC | 120 |
| CTTCAAGGGA GTCGACCCCA ACAGCAGGAA TAGCTCCCGA GTTTTGCGGC CTCCAGGTGG | 180 |
| TGGATCCAAT TTTTCATTAG GTTTTGATGA ACCAACAGAA CAACCTGTGA GGAAGAACAA | 240 |

AATGGCCTCT AATATCTTTG GGACACCTGA AGAAAATCAA GCTTCTTGGG CCAAGTCAGC 300
 AGGTGCCAAG TCTAGTGGTG GCAGGGAAGA CTTGGAGTCA TCTGGACTGC AGAGAAGGAA 360
 CTCCTCTGAA GCAAGCTCCG GAGACTTCTT AGATCTGAAG GGAGAAGGTG ATATTCATGA 420
 AAATGTGGAC ACAGACTTGC CAGGCAGCCT GGGGCAGAGT GAAGAGAAGC CCGTGCCTGC 480
 TGCGCCTGTG CCCAGCCCGG TGGCCCCGGC CCCAGTGCCA TCCAGAAGAA ATCCCCCTGG 540
 CGGCAAGTCC AGCCTCGTCT TGGGTTAGCT CTGACTGTCC TGAACGCTGT CGTTCTGTCT 600
 GTTTCCTCCA TGCTTGTGAA CTGCACAACT TGAGCCTGAC TGTACATCTC TTGGATTTGT 660
 TTCATTAAAA AGAAGCACTT TATGTACTGC TGTCTTTTTT TTTTTTCTT TTGAAGAACA 720
 GGTTTCTCTC TGTCCTTGAC TCTTGGGTCT GTGGGCCATG GCATGAGTGT TTTCTAGTAG 780
 TAGATTGGAG GGAAAGCTTT GTGACACTTA GTACTGTGTT TTTAAGAAGA AATAATTTGG 840
 TTCCAGATGT GTTAGAGGAT CTTTTGTACT GAGGTTTTTA ACACTTTACT TGGGTTTACC 900
 AAGCCTCAAC TGGACAGACC ATAAACAGTC CACAGGCACC GTTCCTGCCA GGCCCCAACC 960
 CACAGGGAGT CTCTCCGCAG AGCCTTCTTG GTGTTGCCCT AACTTGCCAG TGGCCTTTGC 1020
 TCAGAGCCTC CTCCTGTGAC ATGTGAACAA TGAAGAGGCC TGCGCYTCCT GCCTTGCCGC 1080
 CTGCAAAGCA AAGAACTGC CTTTTATTTT TTAACCTTAA AAAGTAGCCA GATAGTAACA 1140
 AGACTGGCTG GCTGATGAGC AAAGCYTTTG CTCTCACGCA GAGGAAGGCT TGGATGTACA 1200
 ATGAAACTGC CTGGAATAA AAGCAGTGAA GCAAGGGAGG CAATCACACT GAAGCGGGTC 1260
 TTCCTCCAGG AACGGGGTCC CACAGGCGTG TTGTTTTAAA TAACCTGATG CTGTGTGCAT 1320
 GATGCTGGTG CTTGACCATG AAAGGAAAGT CTCATCCTTA AAATGTGTTG TACTTCACAA 1380
 TCCTGGACTG TTGCTTCAAG TAAACAATAT CCACATTTTG AAAAAAAAAA AAAAA 1435

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Met Thr Thr Thr Thr Thr Phe Lys Gly Val Asp Pro Asn Ser Arg Asn

| | | | |
|---|-----|-----|----|
| 1 | 5 | 10 | 15 |
| Ser Ser Arg Val Leu Arg Pro Pro Gly Gly Gly Ser Asn Phe Ser Leu | | | |
| 20 | 25 | 30 | |
| Gly Phe Asp Glu Pro Thr Glu Gln Pro Val Arg Lys Asn Lys Met Ala | | | |
| 35 | 40 | 45 | |
| Ser Asn Ile Phe Gly Thr Pro Glu Glu Asn Gln Ala Ser Trp Ala Lys | | | |
| 50 | 55 | 60 | |
| Ser Ala Gly Ala Lys Ser Ser Gly Gly Arg Glu Asp Leu Glu Ser Ser | | | |
| 65 | 70 | 75 | 80 |
| Gly Leu Gln Arg Arg Asn Ser Ser Glu Ala Ser Ser Gly Asp Phe Leu | | | |
| 85 | 90 | 95 | |
| Asp Leu Lys Gly Glu Gly Asp Ile His Glu Asn Val Asp Thr Asp Leu | | | |
| 100 | 105 | 110 | |
| Pro Gly Ser Leu Gly Gln Ser Glu Glu Lys Pro Val Pro Ala Ala Pro | | | |
| 115 | 120 | 125 | |
| Val Pro Ser Pro Val Ala Pro Ala Pro Val Pro Ser Arg Arg Asn Pro | | | |
| 130 | 135 | 140 | |
| Pro Gly Gly Lys Ser Ser Leu Val Leu Gly | | | |
| 145 | 150 | | |

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1904 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

| | |
|---|-----|
| CAGCGTCGCG CGCGCTACCA CACCCAGGTT CGGCCCGTAG GCGTCTGGCA GCCCGGCGCC | 60 |
| ATCTTCATCG AGCGCCATGG CCGCAGCCTG CGGGCCGGGA GCGGCCGGGT ACTGCTTGCT | 120 |
| CCTCGGCTTG CATTTGTTTC TGCTGACCGC GGGCCCTGCC CTGGGCTGGA ACGACCCTGA | 180 |
| CAGAATGTTG CTGCGGGATG TAAAAGCTCT TACCCTCCAC TATGACCGCT ATACCACCTC | 240 |
| CCGCAGGCTG GATCCCATCC CACAGTTGAA ATGTGTTGGA GGCACAGCTG GTTGTGATTG | 300 |
| TTATACCCCA AAAGTCATAC AGTGTCAGAA CAAAGGCTGG GATGGGTATG ATGTACAGTG | 360 |
| GGAATGTAAG ACGGACTTAG ATATTGCATA CAAATTTGGA AAAACTGTGG TGAGCTGTGA | 420 |

AGGCTATGAG TCCTCTGAAG ACCAGTATGT ACTAAGAGGT TCTTGTGGCT TGGAGTATAA 480
TTTAGATTAT ACAGAACTTG GCCTGCAGAA ACTGAAGGAG TCTGGAAAGC AGCACGGCTT 540
TGCCTCTTTC TCTGATTATT ATTATAAGTG GTCCTCGGCG GATTCCTGTA ACATGAGTGG 600
ATTGATTACC ATCGTGGTAC TCCTTGGGAT CGCCTTTGTA GTCTATAAGC TGTTCTGAG 660
TGACGGGCAG TATTCTCCTC CACCGTACTC TGAGTATCCT CCATTTTCCC ACCGTTACCA 720
GAGATTCACC AACTCAGCAG GACCTCCTCC CCCAGGCTTT AAGTCTGAGT TCACAGGACC 780
ACAGAATACT GGCCATGGTG CAACTTCTGG TTTTGGCAGT GCTTTTACAG GACAACAAGG 840
ATATGAAAAT TCAGGACCAG GGTTCCTGGAC AGGCTTGGGA ACTGGTGGAA TACTAGGATA 900
TTTGTTTGGC AGCAATAGAG CGGCAACACC CTTCTCAGAC TCGTGGTACT ACCCGTCTTA 960
TCCTCCCTCC TACCCTGGCA CGTGGAATAG GGCTTACTCA CCCCTTCATG GAGGCTCGGG 1020
CAGCTATTCTG GTATGTTCAA ACTCAGACAC GAAAACCAGA ACTGCATCAG GATATGGTGG 1080
TACCAGGAGA CGATAAAGTA GAAAGTTGGA GTCAAACACT GGATGCAGAA ATTTTGGATT 1140
TTTCATCACT TTCTCTTTAG AAAAAAAGTA CTACCTGTTA ACAATTGGGA AAAGGGGATA 1200
TTCAAAAGTT CTGTGGTGTT ATGTCCAGTG TAGCTTTTTG TATTCTATTA TTTGAGGCTA 1260
AAAGTTGATG TGTGACAAAA TACTTATGTG TTGTATGTCA GTGTAACATG CAGATGTATA 1320
TTGCAGTTTT KGAAAGTGAT CATTACTGTG GAATGCTAAA AATACATTAA TTTCTAAAC 1380
CTGTGATGCC CTAAGAAGCA TTAAGAATGA AGGTGTTGTA CTAATAGAAA CTAAGTACAG 1440
AAAATTTTCTG TTTTAGGTGG TTGTAGCTGA TGAGTTATTA CCTCATAGAG ACTATAATAT 1500
TCTATTTGGT ATTATATTAT TTGATGTTTG CTGTTCTTCA AACATTTAAA TCAAGCTTTG 1560
GACTAATTAT GCTAATTTGT GAGTTCTGAT CACTTTTGAG CTCTGAAGCT TTGAATCATT 1620
CAGTGGTGGA GATGGCCTTC TGGTAACTGA ATATTACCTT CTGTAGGAAA AGGTGGAAAA 1680
TAAGCATCTA GAAGGTTGTT GTGAATGACT CTGTGCTGGC AAAAATGCTT GAAACCTCTA 1740
TATTTCTTTC GTTCATAAGA GGTAAAGGTC AAATTTTTC ACAAAGTCT TTTAATAACA 1800
AAAGCATGCA GTTCTCTGTG AAATCTCAAA TATTGTTGTA ATAGTCTGTT TCAATCTTAA 1860
AAAGAATCAA TAAAAACAAA CAAGGAAAAA AAAAAAAAAA AAAA 1904

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```

Met Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu
1           5           10           15

Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn
20           25           30
Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His
35           40           45

Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu
50           55           60

Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val
65           70           75           80

Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu
85           90           95

Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val
100          105          110

Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly
115          120          125

Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln
130          135          140

Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp
145          150          155          160

Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu
165          170          175

Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu
180          185          190

Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro
195          200          205

Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro
210          215          220

Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His
225          230          235          240

Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr
245          250          255

Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile

```

| | | |
|---|-----|-----|
| 260 | 265 | 270 |
| Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp | | |
| 275 | 280 | 285 |
| Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn | | |
| 290 | 295 | 300 |
| Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys | | |
| 305 | 310 | 315 |
| 320 | | |
| Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr | | |
| 325 | 330 | 335 |
| Arg Arg Arg | | |

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1260 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

| | |
|---|-----|
| CTGTCTGGCG GCGGCAGCAT GCGGCGGGG GCGGCTGAGG CAGCTGTAGC GGCCGTGGAG | 60 |
| GAGGTCGGCT CAGCCGGGCA GTTTGAGGAG CTGCTGCGCC TCAAAGCCAA GTCCCTCCTT | 120 |
| GTGGTCCATT TCTGGGCACC ATGGGCTCCA CAGTGTGCAC AGATGAACGA AGTTATGGCA | 180 |
| GAGTTAGCTA AAGAACTCCC TCAAGTTTCA TTTGTGAAGT TGGAAGCTGA AGGTGTTCTT | 240 |
| GAAGTATCTG AAAAATATGA AATTAGCTCT GTTCCCACTT TTCTGTTTTT CAAGAATTCT | 300 |
| CAGAAAATCG ACCGATTAGA TGGTGCACAT GCCCCAGAGT TGACCAAAAA AGTTCAGCGA | 360 |
| CATGCATCTA GTGGCTCCTT CCTACCCAGC GCTAATGAAC ATCTTAAAGA AGACCTCAGC | 420 |
| CTTCGCCTGA AAAAGCTGAC TCACGCTGCC CCCTGCATGC TGTTCATGAA GGGAACACCT | 480 |
| CAAGAACCAC GCTGTGGTTT CAGCAAGCAG ATGGTGGAAA TCCTTCACAA ACACAATATT | 540 |
| CAGTTCAGCA GCTTTGATAT CTTCTCAGAT GAAGAAGTTC GACAGGGGCT CAAAACGTAC | 600 |
| TCTAATTGGC CCACCTATCC TCAGCTCTAT GTTTCTGGAG AGCTAATAGG AGGACTTGAC | 660 |
| ATAATTAAGG AGCTGGAAGC ATCAGAAGAG CTGGACACGA TCTGTCCCAA AGCTCCCCAA | 720 |
| TTAGAGGAAA GGCTCAAAGT GCTGACAAAT AAAGCTTCTG TGATGCTCTT TATGAAAGGA | 780 |

AACAAACAGG AAGCAAAATG TGGATTCAGC AAACAAATTC TGGAAATACT AAATAGTACT 840
GGTGTGTAAT ATGAAACATT CGATATATTG GAGGATGAAG AAGTTCGGCA AGGATTAAAA 900
GCTTACTCAA ATTGGCCAAC ATACCCTCAG CTGTATGTGA AAGGGGAGCT GGTGGGAGGA 960
TTGGATATTG TGAAGGAACT GAAAGAAAAT GGTGAATTGC TGCCTATACT GAGAGGAGAA 1020
AATTAATAAA TCTTAAACTT GGTGCCCAAC TATTGTAAGA AATATTTAAT TACATTGGGA 1080
GCAGTTCATG ATTTAGTCCT CAGAAATGGA CTAGGAATAG AAAATTCCTG CTTTCTCAGT 1140
TACATGTTTT GTGTATTTCA CAATGTCGTG CTAAATAAAT GTATGTTACA TTTTTTTCCC 1200
ACCAAAAATA GAATGCAATA AACATCTTCA AATTATTAAC AATAAAAAAA AAAAAAAAAA 1260

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met Ala Ala Gly Ala Ala Glu Ala Ala Val Ala Ala Val Glu Glu Val
1 5 10 15
Gly Ser Ala Gly Gln Phe Glu Glu Leu Leu Arg Leu Lys Ala Lys Ser
20 25 30
Leu Leu Val Val His Phe Trp Ala Pro Trp Ala Pro Gln Cys Ala Gln
35 40 45
Met Asn Glu Val Met Ala Glu Leu Ala Lys Glu Leu Pro Gln Val Ser
50 55 60
Phe Val Lys Leu Glu Ala Glu Gly Val Pro Glu Val Ser Glu Lys Tyr
65 70 75 80
Glu Ile Ser Ser Val Pro Thr Phe Leu Phe Phe Lys Asn Ser Gln Lys
85 90 95
Ile Asp Arg Leu Asp Gly Ala His Ala Pro Glu Leu Thr Lys Lys Val
100 105 110
Gln Arg His Ala Ser Ser Gly Ser Phe Leu Pro Ser Ala Asn Glu His
115 120 125

Leu Lys Glu Asp Leu Ser Leu Arg Leu Lys Lys Leu Thr His Ala Ala
130 135 140

Pro Cys Met Leu Phe Met Lys Gly Thr Pro Gln Glu Pro Arg Cys Gly
145 150 155 160

Phe Ser Lys Gln Met Val Glu Ile Leu His Lys His Asn Ile Gln Phe
165 170 175

Ser Ser Phe Asp Ile Phe Ser Asp Glu Glu Val Arg Gln Gly Leu Lys
180 185 190

Thr Tyr Ser Asn Trp Pro Thr Tyr Pro Gln Leu Tyr Val Ser Gly Glu
195 200 205

Leu Ile Gly Gly Leu Asp Ile Ile Lys Glu Leu Glu Ala Ser Glu Glu
210 215 220

Leu Asp Thr Ile Cys Pro Lys Ala Pro Lys Leu Glu Glu Arg Leu Lys
225 230 235 240

Val Leu Thr Asn Lys Ala Ser Val Met Leu Phe Met Lys Gly Asn Lys
245 250 255

Gln Glu Ala Lys Cys Gly Phe Ser Lys Gln Ile Leu Glu Ile Leu Asn
260 265 270

Ser Thr Gly Val Glu Tyr Glu Thr Phe Asp Ile Leu Glu Asp Glu Glu
275 280 285

Val Arg Gln Gly Leu Lys Ala Tyr Ser Asn Trp Pro Thr Tyr Pro Gln
290 295 300

Leu Tyr Val Lys Gly Glu Leu Val Gly Gly Leu Asp Ile Val Lys Glu
305 310 315 320

Leu Lys Glu Asn Gly Glu Leu Leu Pro Ile Leu Arg Gly Glu Asn
325 330 335

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1152 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ACTTTTTCG ATGCCTACTG GAGACTTTGA TTCGAAGCCC AGTTGGGCCG ACCAGGTGGA 60

GGAGGAGGGG GAGGACGACA AATGTGTAC CAGCGAGCTC CTCAAGGGGA TCCCTCTGGC 120

CACAGGTGAC ACCAGCCCAG AGCCAGAGCT ACTGCCGGGA GCTCCACTGC CGCCTCCCAA 180
GGAGGTCATC AACCGAAACA TAAAGACAGT GACAGAGTAC AAGATAGATG AGGATGGCAA 240
GAAGTTCAAG ATTGTCCGCA CCTTCAGGAT TGAGACCCGG AAGGCTTCAA AGGCTGTCGC 300
AAGGAGGAAG AACTGGAAGA AGTTCGGGAA CTCAGAGTTT GACCCCCCCG GACCCAATGT 360
GGCCACCACC ACTGTCAGTG ACGATGTCTC TATGACGTTT ATCACCAGCA AAGAGGACCT 420
GAACTGCCAG GAGGAGGAGG ACCCTATGAA CAAACTCAAG GGCCAGAAGA TCGTGTCTTG 480
CCGCATCTGC AAGGGCGACC ACTGGACCAC CCGCTGCCCC TACAAGGATA CGCTGGGGCC 540
CATGCAGAAG GAGCTGGCCG AGCAGCTGGG CCTGTCTACT GGCGAGAAGG AGAAGCTGCC 600
GGGAGAGCTA GAGCCGGTGC AGGCCACGCA GAACAAGACA GGAAGTATG TGCCGCCGAG 660
CCTGCGCGAC GGGGCCAGCC GCCGCGGGGA GTCCATGCAG CCCACCCGCA GAGCCGACGA 720
CAACGCCACC ATCCGTGTCA CCAACTTGTC AGAGGACACG CGTGAGACCG ACCTGCAGGA 780
GCTCTTCCGG CCTTTCGGCT CCATCTCCCG CATCTACCTG GCTAAGGACA AGACCACTGG 840
CCAATCCAAG GGCTTCGCCT TCATCAGCTT CCACCGCCGC GAGGATGCTG CGCGTGCCAT 900
TGCCGGGGTG TCCGGCTTTG GCTACGACCA CCTCATCTC AACGTCGAGT GGGCCAAGCC 960
GTCCACCAAC TAAGCCAGCT GCCACCGTGT ACTCGGTCCG GGACCCTTGG CGACAGAAGA 1020
CAGCCTCCGA GAGCGCGGGC TCCAAGGGCA ATAAAGCAGC TCCACTCTCA AAAAAAAAAA 1080
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1140
AAAAAAAAA AA 1152

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Met Pro Thr Gly Asp Phe Asp Ser Lys Pro Ser Trp Ala Asp Gln Val
1 5 10 15

Glu Glu Glu Gly Glu Asp Asp Lys Cys Val Thr Ser Glu Leu Leu Lys
20 25 30

Gly Ile Pro Leu Ala Thr Gly Asp Thr Ser Pro Glu Pro Glu Leu Leu
35 40 45

Pro Gly Ala Pro Leu Pro Pro Pro Lys Glu Val Ile Asn Gly Asn Ile
50 55 60

Lys Thr Val Thr Glu Tyr Lys Ile Asp Glu Asp Gly Lys Lys Phe Lys
65 70 75 80

Ile Val Arg Thr Phe Arg Ile Glu Thr Arg Lys Ala Ser Lys Ala Val
85 90 95

Ala Arg Arg Lys Asn Trp Lys Lys Phe Gly Asn Ser Glu Phe Asp Pro
100 105 110

Pro Gly Pro Asn Val Ala Thr Thr Thr Val Ser Asp Asp Val Ser Met
115 120 125

Thr Phe Ile Thr Ser Lys Glu Asp Leu Asn Cys Gln Glu Glu Glu Asp
130 135 140

Pro Met Asn Lys Leu Lys Gly Gln Lys Ile Val Ser Cys Arg Ile Cys
145 150 155 160

Lys Gly Asp His Trp Thr Thr Arg Cys Pro Tyr Lys Asp Thr Leu Gly
165 170 175

Pro Met Gln Lys Glu Leu Ala Glu Gln Leu Gly Leu Ser Thr Gly Glu
180 185 190

Lys Glu Lys Leu Pro Gly Glu Leu Glu Pro Val Gln Ala Thr Gln Asn
195 200 205

Lys Thr Gly Lys Tyr Val Pro Pro Ser Leu Arg Asp Gly Ala Ser Arg
210 215 220

Arg Gly Glu Ser Met Gln Pro Thr Arg Arg Ala Asp Asp Asn Ala Thr
225 230 235 240

Ile Arg Val Thr Asn Leu Ser Glu Asp Thr Arg Glu Thr Asp Leu Gln
245 250 255

Glu Leu Phe Arg Pro Phe Gly Ser Ile Ser Arg Ile Tyr Leu Ala Lys
260 265 270

Asp Lys Thr Thr Gly Gln Ser Lys Gly Phe Ala Phe Ile Ser Phe His
275 280 285

Arg Arg Glu Asp Ala Ala Arg Ala Ile Ala Gly Val Ser Gly Phe Gly
290 295 300

Tyr Asp His Leu Ile Leu Asn Val Glu Trp Ala Lys Pro Ser Thr Asn
305 310 315 320

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1594 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

| | |
|---|------|
| CTGAGACCTG GGCTGCTGTG AAAGCCCCTG CACAATCAGC CAGGGAGAAC TGGGCGGGTT | 60 |
| TAGTGGCCCC AGGCCCACTC CTCATGCAGC AGTGTGCTGG GGCGACAGCT CGTCTCCCCT | 120 |
| CTCTTAAGCA CCCGCTTCCT CACCACCCCC ACTGTTGGGC CTATAGTAGC AGGTTAGTGA | 180 |
| GTACCTAGGG CGGCTCAACT CCTCCCACAG CACCAACCCA GCATGGTCCC ACTGAAGTCC | 240 |
| TACTACGCCC TCCCCTCCCC AGCCTTTTCC AGAAACCATA CTGGGCTCAG ATCAGAGCTC | 300 |
| CGAAGCGGTC AAAGTGAGCT GAGCAGGACA GGCCCAGCCT TTCTCCACTG CCACGTCCCT | 360 |
| CATGCACATC ACTCATCTCC TGCTGCAGGC CAAGGCCAAA ATTGGGCTAG TCCTGGCCAG | 420 |
| GGAAATCAGA AGCTCTTCTT GGGTGAGATT GAGCCTCCTG TTGCTCCCTG GAGTTCCGGA | 480 |
| GGCTGGGCTG CAGCCCCTC AGCTTGCGGG CAAAATACGT GCTCTCCTCT CTCCTTGTC | 540 |
| GCTGAGCAAA CCCAGGGAAT AGCCCTCCTC TCCCAGGAA ACTTCTCTGA AATCTTAGAC | 600 |
| TTAGCCAGTC TTAGGCCTAC GATGCCACAC AAAGGTTGTT CAGGGAGAAG GGGGTGCAGG | 660 |
| AGGCAGAGGG TGCCCCGAG GGAGCTGGTG GCTCCAGCCC CACTAGAGCT CCTAAAGATC | 720 |
| ACACAGCAGC TGCTCCTGAC AGGGATGCTC ATGCCAGAA AGCAAGCCCA GGAGAGGAAG | 780 |
| GCAGAGTGTG ACAGAGCAGA GCCAGGGCCA GGCGCACCAG GAGAGGCGTT TCTGGGGCTC | 840 |
| CAGGGAAGTG CCACGGGAGG CAGAAGTCCA GAACTGCCCC TATAGATGCC CTTCTACATC | 900 |
| CTGGAGCCCA AATCAGTCAT GTGGGTGGGA AGTCCCAGG GCAGTGGTCA CATCGTGAGA | 960 |
| ATTAGCAGGA AAGGCGGGGC CTTTCTTGTC ATAGCTATTT CTGAGGATGA AATGGGAGAC | 1020 |
| ATATGCCAG CACCTGATGT AAGTTTATAT AATGTACCTA CACTAAGAA ATACATGAAC | 1080 |
| CGTGCCATGA GGACAGTAAG TGTTCATAAA GCAACATGAA GCAAGAAACA GTGCAGGGTG | 1140 |
| CCCAGTGCAC AACTAGAGA GAAATTGTGA ACATTAAGGA CAAGGAGAAT TGGTGTCTTT | 1200 |
| CTAAACATA CTTATTTAAA AACACATACC CACTTACTAA TGTGGAATTA CACAGTTTGT | 1260 |
| AACAAGAAAA CAGTCTCTCC CATTCTCTAG TACTGYTCCC CTACCCAGCA GTCAMTTCCA | 1320 |
| GTTCAATCAG STATTTTAA AATGTGCTTA TATGACTCTT GCTTGATATA TCAATYTTAG | 1380 |

ACATTACCTG TTGACTCCCT GTTGTACATC ATGAGGCTTT AGCTCTYTTT TGTCAGCAAC 1440
 CCTCCCCCAT CCCTAGTTAT TAGGTTAAAA AATACTCAGA TTACTATTTT TATTACTATG 1500
 TGAAAGTTAA CTGCGGAGCC AAGAGTTGGA CTATAATTAA ATTACCTTCC TTGTAAAAAA 1560
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA 1594

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Pro | Leu | Lys | Ser | Tyr | Tyr | Ala | Leu | Pro | Ser | Pro | Ala | Phe | Ser | 1 | 5 | 10 | 15 |
| Arg | Asn | His | Thr | Gly | Leu | Arg | Ser | Glu | Leu | Arg | Ser | Gly | Gln | Ser | Glu | 20 | 25 | 30 | |
| Leu | Ser | Arg | Thr | Gly | Pro | Ala | Phe | Leu | His | Cys | His | Val | Pro | His | Ala | 35 | 40 | 45 | |
| His | His | Ser | Ser | Pro | Ala | Ala | Gly | Gln | Gly | Gln | Asn | Trp | Ala | Ser | Pro | 50 | 55 | 60 | |
| Gly | Gln | Gly | Asn | Gln | Lys | Leu | Phe | Leu | Gly | Glu | Ile | Glu | Pro | Pro | Val | 65 | 70 | 75 | 80 |
| Ala | Pro | Trp | Ser | Ser | Gly | Gly | Trp | Ala | Ala | Ala | His | Ser | Ala | Cys | Gly | 85 | 90 | 95 | |
| Gln | Asn | Thr | Cys | Ser | Pro | Leu | Ser | Leu | Ser | Ala | Glu | Gln | Thr | Gln | Gly | 100 | 105 | 110 | |
| Ile | Ala | Leu | Leu | Ser | Pro | Gly | Asn | Phe | Ser | Glu | Ile | Leu | Asp | Leu | Ala | 115 | 120 | 125 | |
| Ser | Leu | Arg | Pro | Thr | Met | Pro | His | Lys | Gly | Cys | Ser | Gly | Arg | Arg | Gly | 130 | 135 | 140 | |
| Cys | Arg | Arg | Gln | Arg | Val | Pro | Arg | Arg | Glu | Leu | Val | Ala | Pro | Ala | Pro | 145 | 150 | 155 | 160 |
| Leu | Glu | Leu | Leu | Lys | Ile | Thr | Gln | Gln | Leu | Leu | Leu | Thr | Gly | Met | Leu | 165 | 170 | 175 | |
| Met | Pro | Arg | Lys | Gln | Ala | Gln | Glu | Arg | Lys | Ala | Glu | Cys | Asp | Arg | Ala | 180 | 185 | 190 | |

Glu Pro Gly Pro Gly Ala Pro Gly Glu Ala Phe Leu Gly Leu Gln Gly
195 200 205

Ser Ala Thr Gly Gly Arg Ser Pro Glu Leu Pro Ile
210 215 220

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

TNAATAAACTG GACGGATGCA CTGATAGG

29

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

CNCTGATAACA AAGCATTGCC ACTGGCGC

29

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

TNATCCAGAAA ATTACCGCCG TCCGACCG

29

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

CNCTTAGAAGC CTTCATTTTG GGAAGTC

29

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

CNGAGAAGACT CAACGAGGCA GCCAAGAA

29

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CNTGCTGACTT GGCCAAGAA GCTTGATT

29

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GNGCTGCTTTC CAGACTCCTT CAGTTTCT

29

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ANCCACAGCGT GGTTCCTTGAG GTGTTCCC

29

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonulceotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GNTCTTCTGGC CCTTGAGTTT GTTCATAG

29

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GNTGAGCCGCC CTAGGTACTC ACTAACCT

29

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1480 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

| | |
|--|------|
| AGGCGCCCTC CCTTCCTGAG GAGCTGTTGG CCTGGGTGGG CAGGAACTGC AGTATGGCCA | 60 |
| TGGGCTGAGC AGGCTGAGCA CCTCAGCCTT TAGGGCTTAT GGCCAGGGGA CACTGTATGA | 120 |
| CTCTCCTCTC CTGCAGGTGT CTATCCACCT GGGGTATGGC ATCTACCGAC CTGTCTCCCT | 180 |
| GGGGTCACAT GCTTTGTTTC CATTCTTGTC CTGGCTGGAC CAGCCACTGT GGGACCAACA | 240 |
| CCCCTCCCAC ACTCCCCAG ACTGCTCGTC TATCACCAGG ATCGCTTTGT ACTTTGTGCA | 300 |
| AAAGGTCTG GCTGTCCCTT GCTGTTTTCA TCTCTGCCAA GCCTATTGTG CCTCTGGCTG | 360 |
| CTGTATGTGT GCGCGTGCAC GTGTGTGTGT TTCATCTGTT CATTCACTGC ACAAGATATT | 420 |
| TATTGAGTGC CCACTACGTG CCAGGCACTG TTGCTGAGTT CCTGTGGGTG TGTCTCTCGA | 480 |
| TGCCACTCCT GCTTCTCTGG GGGCCTCTTT CTGTGCTTCT CTTTGTCCCC AAATTGCTAC | 540 |
| CTCTTTGTCA GTCTGGGTGT CTCAGGTTCT GTGTGTCCTT GTGTGCATTT CTGTCTCTCT | 600 |
| CTGTCCCTCGT CTCTCTGCAA GGCCCTCTAT TTCTCTCTTT CTTGGTGTCT GTCCTTTGCC | 660 |
| CCCTGTGCCC TCTGGATTCT CTGGGTCTAT GTAGGCCCTT GGTCTGCCCT GGGCTCATCA | 720 |
| GCCTTCCTGA CCTCCTCCTG CCCTCCCCTT CACTCCCCTC CTGGCTCTGC CAGTCGGTTC | 780 |
| CCACGGAGCC ATTTTCTAGCT CTGATCAGCA TGGGAATGTG CCTCGGCCTC CAAGGGGCTT | 840 |
| TGTCCTGGTG CCCCCGCCCC TGGTCCCAAC CTGATCCCAC GAGGGAGTTG GGACAGGAGG | 900 |
| ATTGATGGTG CTCCCCTTCC TGCCAGCGTC AGAGGCCCTG GAGAGGGGCT GTCCATGGCA | 960 |
| GCTGGTCTTT ATTCTCCCT CATGAGACA GGGTCGGGGG GTCCCCATTC TTGGAAGAGG | 1020 |
| TTGAGAAGAC TCCTGGGCTT CAGCCTCTCC CACCCAGCCC TGCCCCTCAC CTGCCTGCCC | 1080 |
| TCCCCTCCCC CACTCTATAC TAGGGACTGG ATCTCAGCCT CTGATCAGTT TCACAAAGTT | 1140 |
| TGTTCCCTAA GGAAATCAAA TCCCATTGTC ACCTAACTCT GAAGATCTAA ATAGCCCTTG | 1200 |
| GATCAGTACG GGAACCCCAA ATCCACAGG GCCAGATGTG GAGTCTGTGT CTGCCCCCGT | 1260 |

CTTCTCTCCA TCCTCAAAGC CCCCACTTCT CTCCAGGCTG TTTCTTTTTT TATGACTGTA 1320
AACATAGATA GTGCTTTATT TTGTTAATAA TAAGATAATG ATGAGTAACT TAACCAGCAC 1380
ATTTCTCCTG TTTACACTCG GGGGATTTTT TTGTTTTCTG ATGACATAAT AAAGACAGAT 1440
CATTTCAGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1480

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Arg | Gly | His | Cys | Met | Thr | Leu | Leu | Ser | Cys | Arg | Cys | Leu | Ser | 1 | 5 | 10 | 15 |
| Thr | Trp | Gly | Met | Ala | Ser | Thr | Asp | Leu | Ser | Pro | Trp | Gly | His | Met | Leu | 20 | 25 | 30 | |
| Cys | Phe | His | Ser | Cys | Pro | Gly | Trp | Thr | Ser | His | Cys | Gly | Thr | Asn | Thr | 35 | 40 | 45 | |
| Pro | Pro | Thr | Leu | Pro | Gln | Thr | Ala | Arg | Leu | Ser | Pro | Gly | Ser | Leu | Cys | 50 | 55 | 60 | |
| Thr | Leu | Cys | Lys | Arg | Val | Trp | Leu | Ser | Leu | Ala | Val | Phe | Ile | Ser | Ala | 65 | 70 | 75 | 80 |
| Lys | Pro | Ile | Val | Pro | Leu | Ala | Ala | Val | Cys | Val | Arg | Val | His | Val | Cys | 85 | 90 | 95 | |
| Val | Phe | His | Leu | Phe | Ile | His | Cys | Thr | Arg | Tyr | Leu | Leu | Ser | Ala | His | 100 | 105 | 110 | |
| Tyr | Val | Pro | Gly | Thr | Val | Ala | Glu | Phe | Leu | Trp | Val | Cys | Leu | Ser | Met | 115 | 120 | 125 | |
| Pro | Leu | Leu | Leu | Leu | Trp | Gly | Pro | Leu | Ser | Val | Leu | Leu | Phe | Val | Pro | 130 | 135 | 140 | |
| Lys | Leu | Leu | Pro | Leu | Cys | Gln | Ser | Gly | Cys | Leu | Arg | Phe | Cys | Val | Ser | 145 | 150 | 155 | 160 |
| Leu | Cys | Ala | Phe | Leu | Ser | Leu | Ser | Val | Leu | Val | Ser | Leu | Gln | Gly | Pro | 165 | 170 | 175 | |
| Leu | Phe | Leu | Ser | Phe | Leu | Val | Ser | Val | Leu | Cys | Pro | Leu | Cys | Pro | Leu | | | | |

| | | |
|---|-----|-----|
| 180 | 185 | 190 |
| Asp Ser Leu Gly Leu Cys Arg Pro Leu Val Cys Pro Gly Leu Ile Ser | | |
| 195 | 200 | 205 |
| Leu Pro Asp Leu Leu Leu Pro Ser Pro Ser Leu Pro Pro Trp Leu Cys | | |
| 210 | 215 | 220 |
| Gln Ser Val Pro Thr Glu Pro Phe Leu Ala Leu Ile Ser Met Gly Met | | |
| 225 | 230 | 235 |
| Cys Leu Gly Leu Gln Gly Ala Leu Ser Trp Cys Pro Arg Pro Trp Ser | | |
| 245 | 250 | 255 |
| Gln Pro Asp Pro Thr Arg Glu Leu Gly Gln Glu Asp | | |
| 260 | 265 | |

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

| | |
|---|-----|
| CCCGGCGGCT CCTGGAACCC CGGTTGCGGG CGATGCCAGC CACCCCAGCG AAGCCGCCGC | 60 |
| AGTTCAGTGC TTGGATAATT TGAAAGTACA ATAGTTGGTT TCCCTGTCCA CCCGCCCCAC | 120 |
| TTCGCTTGCC ATCACAGCAC GCCTATCGGA TGTGAGAGGA GAAGTCCCGC TGCTCGGGCA | 180 |
| CTGTCTATAT ACGCCTAACA CCTACATATA TTTTAAAAAC ATTAAATATA ATTAACAATC | 240 |
| AAAAGAAAGA GGAGAAAGGA AGGGAAGCAT TACTGGGTTA CTATGCACTT GCGACTGATT | 300 |
| TCTTGGCTTT TTATCATTTT GAACTTTATG GAATACATCG GCAGCCAAAA CGCCTCCCGG | 360 |
| GGAAGGCGCC AGCGAAGAAT GCATCCTAAC GTTAGTCAAG GCTGCCAAGG AGGCTGTGCA | 420 |
| ACATGCTCAG ATTACAATGG ATGTTTGTCA TGTAAGCCCA GACTATTTTT TGCTCTGGAA | 480 |
| AGAATTGGCA TGAAGCAGAT TGGAGTATGT CTCTCTTCAT GTCCAAGTGG ATATTATGGA | 540 |
| ACTCGATATC CAGATATAAA TAAGTGTAACA AAATGCAAAAG CTGACTGTGA TACCTGTTTC | 600 |
| AACAAAAATT TCTGCACAAA ATGTAAAAGT GGATTTTACT TACACCTTGG AAAGTGCCTT | 660 |
| GACAATTGCC CAGAAGGGTT GGAAGCCAAC AACCATACTA TGGAGTGTGT CAGTATTGTG | 720 |
| CACTGTGAGG TCAGTGAATG GAATCCTTGG AGTCCATGCA CGAAGAAGGG AAAAACATGT | 780 |

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GGCTTCAAAA GAGGGACTGA AACACGGGTC CGAGAAATAA TACAGCATCC TTCAGCAAAG      840
GGTAACCTGT GTCCCCAAC AAATGAGACA AGAAAGTGTA CAGTGCAAAG GAAGAAGTGT      900
CAGAAGGGAG AACGAGGAAA AAAAGGAAGG GAGAGGAAAA GAAAAAACC TAATAAAGGA      960
GAAAGTAAAG AAGCAATACC TGACAGCAAA AGTCTGGAAT CCAGCAAAGA AATCCCAGAG     1020
CAACGAGAAA ACAAACAGCA GCAGAAGAAG CGAAAAGTCC AAGATAAACA GAAATCGGGG     1080
ATTGAAGTCA CCCTAGCTGA AGGCCTCACC AGTGTTCAC AGAGGACACA GCCCACCCT      1140
TGCAGGAGGA GGTATCTCTG AGTGTGCAGC ACAGAATCGC ATGACCCACC TTAACCTTCC     1200
TGTTGTCATG GAAGGATGCA CGGCTGCTCT GTCCACTGTG ATTCCTAGCC CTCTCAAGAT     1260
CACTGCTTTC TGAAGAATTT GCAATGACTC TGGCTTCTGG CTGCTTATCT CTGGACACCC     1320
GTTCTCCACC AGTTGTACAG TTCATGTAAT CTAATTGGCT TAATTGATTT TCCACTTCTC     1380
TCTTCCTCTT CTAAGATATA AACATTTTAA ATGATTTAAA AAAAAAAAAA AAAAAA      1436

```

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

```

Met His Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met
1           5           10           15

Glu Tyr Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg
20           25           30

Met His Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys
35           40           45

Ser Asp Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala
50           55           60

Leu Glu Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys
65           70           75           80

Pro Ser Gly Tyr Tyr Gly Thr Arg Tyr Pro Asp Ile Asn Lys Cys Thr
85           90           95

Lys Cys Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr
100          105          110

Lys Cys Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn

```

| | | |
|---|-----|-----|
| 115 | 120 | 125 |
| Cys Pro Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser | | |
| 130 | 135 | 140 |
| Ile Val His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr | | |
| 145 | 150 | 155 |
| Lys Lys Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val | | |
| | 165 | 170 |
| Arg Glu Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro | | |
| | 180 | 185 |
| Thr Asn Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys | | |
| | 195 | 200 |
| Gly Glu Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn | | |
| 210 | 215 | 220 |
| Lys Gly Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser | | |
| 225 | 230 | 235 |
| Ser Lys Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys | | |
| | 245 | 250 |
| Arg Lys Val Gln Asp Lys Gln Lys Ser Gly Ile Glu Val Thr Leu Ala | | |
| | 260 | 265 |
| Glu Gly Leu Thr Ser Val Ser Gln Arg Thr Gln Pro Thr Pro Cys Arg | | |
| | 275 | 280 |
| Arg Arg Tyr Leu | | |
| 290 | | |

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

| | |
|---|-----|
| GGTTAAGAGC AGATTAGAAC AGAAATCAGG AGAACTTGGG AAGAAGATCA CTGAGTTAAC | 60 |
| ATTGAAAAAT CAGACACTAC AAAAGGAAAT TGAAAAAGTT TATTTGGATA ATAAGCTCCT | 120 |
| CAAGGAGCAA GCACATAACT TAACAATTGA AATGAAAAAT CATTATGTTC CTTTAAAGT | 180 |
| AAGTGAAGAC ATGAAAAAGT CACATGATGC AATTATTGAT GATCTTAATA GAAAGCTTTT | 240 |

| | | | | | | |
|-------------|------------|-------------|-------------|-------------|--------------|------|
| AGATGTAACA | CAAAAATATA | CAGAAAAGAA | GTTGGAAATG | GAGAAATTGC | TACTGGAAAA | 300 |
| TGACAGCTTA | AGTAAGGATG | TAAGCCGCCT | AGAAACTGTG | TTTGTACCTC | CTGAGAAACA | 360 |
| TGAAAAAGAG | ATAATAGCTC | TGAAATCCAA | TATTGTTGAA | CTTAAGAAAC | AGCTGTCTGA | 420 |
| ACTTAAGAAA | AAATGTGGTG | AAGACCAGGA | GAAAAATACAC | GCTCTCACAT | CTGAAAACAC | 480 |
| TAAC TTGAAG | AAGATGATGA | GTAATCAGTA | TGTGCCAGTT | AAAACCCATG | AAGAGGTTAA | 540 |
| AATGACACTG | AATGACACGT | TAGCCAAAAC | TAACAGAGAA | TTATTAGATG | TGAAGAAAAA | 600 |
| ATTTGAAGAT | ATAAATCAGG | AATTTGTAAA | AATAAAAGAT | AAGAATGAAA | TATTA AAAAAG | 660 |
| AAACCTGGAA | AACACTCAGA | ACCAAATAAA | AGCTGAGTAC | ATCAGCCTGG | CAGAGCACGA | 720 |
| GGCAAAGATG | AGCTCGCTAA | GTCAGAGCAT | GAGAAAGGTG | CAGGATAGTA | ATGCTGAAAT | 780 |
| CTTGGCCAAC | TACAGAAAAG | GCCAAGAAGA | GATTGTGACA | CTGCATGCCG | AAATTAAAGC | 840 |
| CCAGAAGAAG | GAGCTCGACA | CAATACAAGA | ATGCATTAAG | GTAAAATATG | CCCCAATTGT | 900 |
| CAGCTTTGAG | GAGTGCGAGA | GAAAATTTAA | AGCAACAGAG | AAAGAACTAA | AAGACCAGTT | 960 |
| ATCAGAGCAG | ACACAAAAGT | ATAGTGTCAG | TGAAGAAGAA | GTCAAGAAAA | ACAAGCAAGA | 1020 |
| GAATGACAAG | TTAAAGAAGG | AGATTTTTTAC | CCTTCAGAAA | GATTTGAGAG | ATAAGACAGT | 1080 |
| TCTCATTGAG | AAGTCTCATG | AAATGGAAAAG | AGCATTAAGC | AGAAAAACAG | ACGAGCTAAA | 1140 |
| CAAACAGTTA | AAAGACTTGT | CACAGAAATA | CACGGAAGTA | AAGAATGTGA | AAGAGAAGCT | 1200 |
| AGTAGAAGAA | AATGCCAAAC | AGACTTCTGA | GATACTTGCA | GTGCAAAATC | TTTTGCAAAA | 1260 |
| ACAACATGTT | CCATTGGAAC | AGGTTGAGGC | TCTGAAAAAA | TCTCTTAATG | GCACAATTGA | 1320 |
| AAATCTAAAG | GAAGAACTGA | AGAGTATGCA | AAGGTGTTAC | GAGAAAGAGC | AGCAGACAGT | 1380 |
| GACCAAAC TG | CATCAATTGT | TGGAGAATCA | AAAGAACTCT | TCTGTACCCC | TGGCAGAGCA | 1440 |
| TTTG CAGATT | AAAGAAGCAT | TTGAGAAAGA | AGTTGGAATC | ATAAAAGCCA | GCTTGAGAGA | 1500 |
| AAAGGAAGAA | GAAAGCCAAA | ACAAAATGGA | AGAAGTCTCC | AACTTTCAGT | CGGAGGTTCA | 1560 |
| GAATACTAAA | CAAGCATTAA | AAAAATTAGA | GACTAGAGAG | G TAGTTGACT | TGTCTAAATA | 1620 |
| TAAAGCAACA | AAAAGTGATT | TGGAGACACA | GATTTCTAGC | TTAAATGAAA | AATTGGCCAA | 1680 |
| TCTGAATAGA | AAGTATGAGG | AAGTATGTGA | GGAAGTTTTG | CATGCCAAAA | AGAAGGAAAT | 1740 |
| ATCTGCAAAA | GATGAGAAGG | AATTACTGCA | TTTCAGCATT | GAGCAAGAAA | TTAAGGATCA | 1800 |
| GAAGGAACGA | TGTGATAAGT | CCTTAACAAC | AATCACAGAG | TTACAAAGAA | GAATACAAGA | 1860 |
| ATCTGCTAAA | CAAATAGAAG | CAAAAGATAA | TAAGATAACT | GAAGTGCTTA | ATGATGTGGA | 1920 |
| AAGATTAAAA | CAGGCACTCA | ATGGCCTTTC | CCAAC TCACC | TACACAAGTG | GGAACCCAC | 1980 |

CAAGAGGCAG AGCCAGCTGA TTGACACTCT GCAGCACCAA GTGAAATCTC TGGAGCAACA 2040
 GCTGGCCGAT GCTGACAGAC AGCACCAAGA AGTAATTGCA ATTTATCGGA CACACCTTCT 2100
 TAGTGCTGCA CAGGGTCACA TGGATGAAGA TGTTTCAGGAG GCTCTGCTCC AGATCATACA 2160
 AATGCGGCAG GGGCTTGTGT GCTAGCCGTT AGCACTGACT GCCAGTATCT GTTTTATCTT 2220
 GCTGGTGCTG AACATTCTTT GTGCAACTCC ATGGTCTTTC TGGGCCTTAC TGTGCTGGTA 2280
 TAATTAAAAT AAAATATATT TTGTTCTAAA AAAAAAAAAA AA 2322

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 677 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Asn | His | Tyr | Val | Pro | Leu | Lys | Val | Ser | Glu | Asp | Met | Lys | Lys | 1 | 5 | 10 | 15 |
| Ser | His | Asp | Ala | Ile | Ile | Asp | Asp | Leu | Asn | Arg | Lys | Leu | Leu | Asp | Val | 20 | 25 | 30 | |
| Thr | Gln | Lys | Tyr | Thr | Glu | Lys | Lys | Leu | Glu | Met | Glu | Lys | Leu | Leu | Leu | 35 | 40 | 45 | |
| Glu | Asn | Asp | Ser | Leu | Ser | Lys | Asp | Val | Ser | Arg | Leu | Glu | Thr | Val | Phe | 50 | 55 | 60 | |
| Val | Pro | Pro | Glu | Lys | His | Glu | Lys | Glu | Ile | Ile | Ala | Leu | Lys | Ser | Asn | 65 | 70 | 75 | 80 |
| Ile | Val | Glu | Leu | Lys | Lys | Gln | Leu | Ser | Glu | Leu | Lys | Lys | Lys | Cys | Gly | 85 | 90 | 95 | |
| Glu | Asp | Gln | Glu | Lys | Ile | His | Ala | Leu | Thr | Ser | Glu | Asn | Thr | Asn | Leu | 100 | 105 | 110 | |
| Lys | Lys | Met | Met | Ser | Asn | Gln | Tyr | Val | Pro | Val | Lys | Thr | His | Glu | Glu | 115 | 120 | 125 | |
| Val | Lys | Met | Thr | Leu | Asn | Asp | Thr | Leu | Ala | Lys | Thr | Asn | Arg | Glu | Leu | 130 | 135 | 140 | |
| Leu | Asp | Val | Lys | Lys | Lys | Phe | Glu | Asp | Ile | Asn | Gln | Glu | Phe | Val | Lys | 145 | 150 | 155 | 160 |

Ile Lys Asp Lys Asn Glu Ile Leu Lys Arg Asn Leu Glu Asn Thr Gln
165 170 175

Asn Gln Ile Lys Ala Glu Tyr Ile Ser Leu Ala Glu His Glu Ala Lys
180 185 190

Met Ser Ser Leu Ser Gln Ser Met Arg Lys Val Gln Asp Ser Asn Ala
195 200 205

Glu Ile Leu Ala Asn Tyr Arg Lys Gly Gln Glu Glu Ile Val Thr Leu
210 215 220

His Ala Glu Ile Lys Ala Gln Lys Lys Glu Leu Asp Thr Ile Gln Glu
225 230 235 240

Cys Ile Lys Val Lys Tyr Ala Pro Ile Val Ser Phe Glu Glu Cys Glu
245 250 255

Arg Lys Phe Lys Ala Thr Glu Lys Glu Leu Lys Asp Gln Leu Ser Glu
260 265 270

Gln Thr Gln Lys Tyr Ser Val Ser Glu Glu Glu Val Lys Lys Asn Lys
275 280 285

Gln Glu Asn Asp Lys Leu Lys Lys Glu Ile Phe Thr Leu Gln Lys Asp
290 295 300

Leu Arg Asp Lys Thr Val Leu Ile Glu Lys Ser His Glu Met Glu Arg
305 310 315 320

Ala Leu Ser Arg Lys Thr Asp Glu Leu Asn Lys Gln Leu Lys Asp Leu
325 330 335

Ser Gln Lys Tyr Thr Glu Val Lys Asn Val Lys Glu Lys Leu Val Glu
340 345 350

Glu Asn Ala Lys Gln Thr Ser Glu Ile Leu Ala Val Gln Asn Leu Leu
355 360 365

Gln Lys Gln His Val Pro Leu Glu Gln Val Glu Ala Leu Lys Lys Ser
370 375 380

Leu Asn Gly Thr Ile Glu Asn Leu Lys Glu Glu Leu Lys Ser Met Gln
385 390 395 400

Arg Cys Tyr Glu Lys Glu Gln Gln Thr Val Thr Lys Leu His Gln Leu
405 410 415

Leu Glu Asn Gln Lys Asn Ser Ser Val Pro Leu Ala Glu His Leu Gln
420 425 430

Ile Lys Glu Ala Phe Glu Lys Glu Val Gly Ile Ile Lys Ala Ser Leu
435 440 445

Arg Glu Lys Glu Glu Glu Ser Gln Asn Lys Met Glu Glu Val Ser Lys
450 455 460

Leu Gln Ser Glu Val Gln Asn Thr Lys Gln Ala Leu Lys Lys Leu Glu
465 470 475 480

Thr Arg Glu Val Val Asp Leu Ser Lys Tyr Lys Ala Thr Lys Ser Asp
485 490 495

Leu Glu Thr Gln Ile Ser Ser Leu Asn Glu Lys Leu Ala Asn Leu Asn
500 505 510

Arg Lys Tyr Glu Glu Val Cys Glu Glu Val Leu His Ala Lys Lys Lys
515 520 525

Glu Ile Ser Ala Lys Asp Glu Lys Glu Leu Leu His Phe Ser Ile Glu
530 535 540

Gln Glu Ile Lys Asp Gln Lys Glu Arg Cys Asp Lys Ser Leu Thr Thr
545 550 555 560

Ile Thr Glu Leu Gln Arg Arg Ile Gln Glu Ser Ala Lys Gln Ile Glu
565 570 575

Ala Lys Asp Asn Lys Ile Thr Glu Leu Leu Asn Asp Val Glu Arg Leu
580 585 590

Lys Gln Ala Leu Asn Gly Leu Ser Gln Leu Thr Tyr Thr Ser Gly Asn
595 600 605

Pro Thr Lys Arg Gln Ser Gln Leu Ile Asp Thr Leu Gln His Gln Val
610 615 620

Lys Ser Leu Glu Gln Gln Leu Ala Asp Ala Asp Arg Gln His Gln Glu
625 630 635 640

Val Ile Ala Ile Tyr Arg Thr His Leu Leu Ser Ala Ala Gln Gly His
645 650 655

Met Asp Glu Asp Val Gln Glu Ala Leu Leu Gln Ile Ile Gln Met Arg
660 665 670

Gln Gly Leu Val Cys
675

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2041 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

TCTCCCCCT CCCCACACA CACTCACAGG CCGGGCATTG ATGGTAATGT ATGCGAGGAA

60

ACAGCAGAGA CTCAGTGATG GCTGTCACGA CCGGAGGGGG GACTCGCAGC CTTACCAGGC 120
 ACTTAAGTAT TCATCGAAGA GTCACCCAG TAGCGGTGAT CACAGACATG AAAAGATGCG 180
 AGACGCCGGA GATCCTTCAC CACCAAATAA AATGTTGCGG AGATCTGATA GTCCTGAAAA 240
 CAAATACAGT GACAGCACAG GTCACAGTAA GGCCAAAAAT GTGCATACTC ACAGAGTTAG 300
 AGAGAGGGAT GGTGGGACCA GTTACTCTCC ACAAGAAAAT TCACACAACC ACAGTGCTCT 360
 TCATAGTTCA AATTCACATT CTTCTAATCC AAGCAATAAC CCAAGCAAAA CTTCAGATGC 420
 ACCTTATGAT TCTGCAGATG ACTGGTCTGA GCATATTAGC TCTTCTGGGA AAAAGTACTA 480
 CTACAATTGT CGAACAGAAG TTTCAACAATG GGAAAAACCA AAAGAGTGGC TTGAAAGAGA 540
 ACAGAGACAA AAAGAAGCAA ACAAGATGGC AGTCAACAGC TTCCCAAAAG ATAGGGATTA 600
 CAGAAGAGAG GTGATGCAAG CAACAGCCAC TAGTGGGTTT GCCAGTGGA AATCTACATC 660
 AGGAGACAAA CCCGTATCAC ATTCTTGCAC AACTCCTTCC ACGTCTTCTG CCTCTGGACT 720
 GAACCCACACA TCTGCACCTC CAACATCTGC TTCAGCGGTC CCTGTTTCTC CTGTTCCACA 780
 GTCGCCAATA CCTCCCTTAC TTCAGGACCC AAATCTTCTT AGACAATTGC TTCCTGCTTT 840
 GCAAGCCACG CTGCAGCTTA ATAATTCTAA TGTGGACATA TCTAAAATAA ATGAAGTTCT 900
 TACAGCAGCT GTGACACAAG CCTCACTGCA GTCTATAATT CATAAGTTTC TTACTGCTGG 960
 ACCATCTGCT TTCAACATAA CGTCTCTGAT TTCTCAAGCT GCTCAGCTCT CTACACAAGC 1020
 CCAGCCATCT AATCAGTCTC CGATGTCTTT AACATCTGAT GCGTCATCCC CAAGATCATA 1080
 TGTTTCTCCA AGAATAAGCA CACCTCAAAC TAACACAGTC CCTATCAAAC CTTTGATCAG 1140
 TACTCCTCCT GTTTCATCAC AGCCAAAGGT TAGTACTCCA GTAGTTAAGC AAGGACCAGT 1200
 GTCACAGTCA GCCACACAGC AGCCTGTAAC TGCTGACAAG CAGCAAGGTC ATGAACCTGT 1260
 CTCTCCTCGA AGTCTTCAGC GCTCAAGCCA GAGAAGTCCA TCACCTGGTC CCAATCATAC 1320
 TTCTAATAGT AGTAATGCAT CAAATGCAAC AGTTGTACCA CAGAATTCTT CTGCCCCGATC 1380
 CACGTGTTCA TTAACGCCTG CACTAGCAGC AACTTCAGT GAAAATCTCA TAAAACACGT 1440
 TCAAGGATGG CCTGCAGATC ATGCAGAGAA GCAGGCATCA AGATTACGCG AAGAAGCGCA 1500
 TAACATGGGA ACTATTCACTA TGTCCGAAAT TTGTACTGAA TTAAAAAATT TAAGATCTTT 1560
 AGTCCGAGTA TGTGAAATTC AAGCAACTTT GCGAGAGCAA AGGATACTAT TTTTGAGACA 1620
 ACAAATTAAG GAACTTGAAA AGCTAAAAAA TCAGAATTCC TTCATGGTGT GAAGATGTGA 1680
 ATAATTGCAC ATGGTTTTGA GAACAGGAAC TGTAATCTG TTGCCCAATC TTAACATTTT 1740

```

TGAGCTGCAT TTAAGTAGAC TTTGGACCGT TAAGCTGGGC AAAGGAAATG ACAAGGGGAC      1800
GGGGTCTGTG AGAGTCAATT CAGGGGAAAAG ATACAAGATT GATTGTGAAA ACCCTTGAAA      1860
TGTAGATTTC TTGTAGATGT ATCCTTCACG TTGTAAATAT GTTTTGTAGA GTGAAGCCAT      1920
GGGAAGCCAT GTGTAACAGA GCTTAGACAT CCAAACTAA TCAATGCTGA GGTGGCTAAA      1980
TACCTAGCCT TTTACATGTA AACCTGTCTG CAAAATTAGC TTTTAAATAA AAAAAAAAAA      2040
A                                                                                   2041

```

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

```

Met Arg Gly Asn Ser Arg Asp Ser Val Met Ala Val Thr Thr Gly Gly
1           5           10           15

Gly Thr Arg Ser Leu Thr Arg His Leu Ser Ile His Arg Arg Val Thr
20           25           30

Pro Val Ala Val Ile Thr Asp Met Lys Arg Cys Glu Thr Pro Glu Ile
35           40           45

Leu His His Gln Ile Lys Cys Cys Gly Asp Leu Ile Val Leu Lys Thr
50           55           60

Asn Thr Val Thr Ala Gln Val Thr Val Arg Pro Lys Met Cys Ile Leu
65           70           75           80

Thr Glu Leu Glu Arg Gly Met Val Gly Pro Val Thr Leu His Lys Lys
85           90           95

Ile His Thr Thr Thr Val Leu Phe Ile Val Gln Ile His Ile Leu Leu
100          105          110

Ile Gln Ala Ile Thr Gln Ala Lys Leu Gln Met His Leu Met Ile Leu
115          120          125

Gln Met Thr Gly Leu Ser Ile Leu Ala Leu Leu Gly Lys Ser Thr Thr
130          135          140

Thr Ile Val Glu Gln Lys Phe His Asn Gly Lys Asn Gln Lys Ser Gly
145          150          155          160

Leu Lys Glu Asn Arg Asp Lys Lys Lys Gln Thr Arg Trp Gln Ser Thr

```

165

170

175

Ala Ser Gln Lys Ile Gly Ile Thr Glu Glu Arg
180 185

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1163 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GCCCTATCCA CTTAATAGAT GCCAATTCAA AGAGGTTAAA TGATTAGACT AAGGCACCTA 60
ACTTATGTGA GTGTCAGGCT TCAATGCCTG TGTTAGAGCT ACTCCTTCAC ACAAATAGT 120
TCAGAACATA GAGAAGGACC AAGGTTAATA AATGATTTTC ATCCCAAACA CTAAACATGA 180
TTGATGGGTA GAGGCTGCCC GAAGTACTGT GTAAAGATGG AATCTGAGAT AGAAGAATGC 240
TGTGGTCAAT TAGTAATTCT TGCCCATGGA GGGATTAGTG ACACATGCCT TGTATATTTG 300
TCATCTGTGG CCTAAACTCT GCCCCTGAAG GTTTGTTTTT TAATTCAGAG GTTTAAATTA 360
ATCTAGCCCA CTTAATAAAA CCAGAGATCC TATGGGAAAT TTAGCCTAAG ACAGTGCTGG 420
AAATTGCCAT ATGTTGATAC AAAGAAGTGT TTGGCCACAT TACAGGTCTC AGACTCAACT 480
GCTATGTGTG ACTGCCGCTC TGTGCCTATG TCTTGCTTTT TTGCTGAGTT CCCTATTTCC 540
ATATCTCCAG GTGAATCCAT GAGAAGCGAG AGGGTGGCTG AGAGGCCTGG GCCTCTGGGA 600
TTCCACCTTG CTATCTCTGC TCTTCAACCA TTGTTTTAGA CTCTGAACAC CAGATCCTCA 660
TATCTGAAAG TGATTTGGAG ACCTGGGCAT CAAGTGCTCT TTTAAGAAGG GGCTATCCCA 720
GAGGACTGTT CAAAAGTCTC ATTCAATAGA GATGTTGGAG TCCCAGAACA AAGTTAGGGA 780
GCAAACCACT AACCTATGCT GGTSGTAACA GAGGATCCTA CAATTACGTT TGTTTTTAAG 840
ACAGGATTTT GCTGTGTTGC CCAGACTGGT CTCAAATCC TGGGTTCAAG AGATCCATCC 900
TCCCACCTCA GTCTCCTGAA AGCTGGGATG ACAGGCACAT GCCACCACAC CTAGCTCCTT 960
ACAACCATTT ATTTTAACTT ATTTCAATTA TAACTGGTAT CTTTCATTTG TATGTGGCAG 1020
CTAGAGATTT ATATAGGATG GAAGTAATTT ATTTTAAATT TAAATATTTT ATGTTGAAC 1080
GTTTGCCTTG TATGGAACAT TTTACTTGGC CAATTCAAAT AAAAATAAAG TCAGCTTTGT 1140

TTGTGACAAA AAAAAAAAAA AAA

1163

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ile | Gln | Arg | Ser | Val | Trp | Pro | His | Tyr | Arg | Ser | Gln | Thr | Gln |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| | | | | | | | | | | | | | | | |
| Leu | Leu | Cys | Val | Thr | Ala | Ala | Leu | Cys | Leu | Cys | Leu | Ala | Phe | Leu | Leu |
| | | | 20 | | | | 25 | | | | | | 30 | | |
| | | | | | | | | | | | | | | | |
| Ser | Ser | Leu | Phe | Pro | Tyr | Leu | Gln | Val | Asn | Pro | | | | | |
| | | | 35 | | | | 40 | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3067 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GCGGTGGCTG | AGGCGGCTGG | GCCTAGGGTG | CAGCGGGCGC | GTCTGCGGCT | GGTGTGGCG | 60 |
| | | | | | | |
| CATCTCTAGA | TCCTTTCCCG | GAGTTCAGTT | ATGGGTGTGA | GAGGTTTGCA | AGGATTTGTG | 120 |
| | | | | | | |
| GGAAGTACCT | GCCACATAT | ATGTACAGTA | GTAAATTTCA | AAGAACTGGC | AGAGCACCAC | 180 |
| | | | | | | |
| CGAAGCAAGT | ATCCTGGATG | TACCCCTACC | ATTGTGGTTG | ATGCCATGTG | TTGTCTCAGA | 240 |
| | | | | | | |
| TATTGGTATA | CTCCAGAATC | TTGGATCTGC | GGTGGCCAGT | GGCGAGAATA | CTTTTCTGCT | 300 |
| | | | | | | |
| TTGCGAGATT | TTGTAAAC | TTTTACGGCA | GCTGGGATCA | AGTTGATATT | CTTCTTTGAT | 360 |
| | | | | | | |
| GGCATGGTGG | AGCAGGATAA | GAGAGATGAA | TGGGTGAAAC | GAAGGCTCAA | GAACAACAGG | 420 |
| | | | | | | |
| GAGATATCCA | GGATTTTCA | TTACATCAAG | TCACACAAGG | AGCAGCCAGG | CAGAAATATG | 480 |
| | | | | | | |
| TTCTTCATCC | CCTCAGGGCT | AGCTGTGTTT | ACACGATTTG | CTCTAAAGAC | ACTGGGCCAG | 540 |
| | | | | | | |
| GAAACTTTGT | GTTCTTTGCA | GGAAGCAGAT | TATGAGGTAG | CTTCCTATGG | CCTCCAGCAT | 600 |

AACTGTCTTG GGATTCTGGG GGAAGACACT GATTACCTAA TCTATGACAC TTGTCCCTAC 660

TTTTCAATTA GCGAGCTCTG CCTAGAGAGC CTGGACACCG TCATGCTCTG CAGAGAGAAG 720

CTCTGTGAGA GTCTGGGCCT CTGTGTGGCC GACCTTCCTC TTCTGGCCTG CCTCCTTGGC 780

GACGACATAA TCCCAGAGGG CATGTTTGAA AGCTTTAGGT ACAAATGCTT ATCGTCCTAC 840

ACCTCTGTAA AAGAGAACTT TGACAAAAAA GGTAACATCA TATTAGCTGT GTCAGACCAT 900

ATATCGAAAG TTCTTTACTT GTATCAAGGT GAGAAAAAAT TAGAAGAGAT ATTACCTCTG 960

GGACCAAACA AAGCTCTTTT TTATAAAGGA ATGGCATCAT ATCTTTTACC AGGACAAAAA 1020

TCTCCATGGT TTTTCCAAAA ACCCAAAGGT GTAATAACTT TGGACAAACA AGTAATATCC 1080

ACGAGTTCAG ACGCCGAATC CAGGGAAGAA GTTCCCATGT GTTCAGATGC TGAATCCAGG 1140

CAAGAAGTTC CCATGTGTAC AGGCCCTGAA TCCAGGCGAG AAGTTCCCGT GTATACAGAT 1200

TCTGAACCCA GGCAAGAAGT TCCCATGTGT TCAGACCCTG AACCAGGCA AGAAGTTCCC 1260

ACATGTACAG GCCCTGAATC CAGGCGAGAA GTTCCCATGT GTTCAGACCC TGAACCCAGG 1320

CAAGAAGTTC CCATGTGTAC AGGCCCTGAA GCCAGGCAAG AAGTTCCCAT GTATACAGAC 1380

TCTGAACCCA GGCAAGAAGT TCCCATGTAT ACAGACTCTG AACCAGGCA AGAAGTTCCC 1440

ATGTATACAG GCTCTGAACC CAGGCAAGAA GTTCCCATGT ATACAGGCCC TGAATCCAGG 1500

CAAGAAGTTC CCATGTATAC AGGCCCTGAA TCCAGGCAAG AAGTTTTAAT ACGGACAGAC 1560

CCTGAATCTA GGCAAGAAAT TATGTGTACA GGCCATGAAT CCAAACAGGA AGTTCCCAT 1620

TGTACAGATC CTATATCCAA GCAAGAAGAC TCCATGTGTA CACACGCTGA AATCAATCAA 1680

AAATTACCTG TAGCAACAGA TTTTGAATTT AAGCTAGAAG CTCTCATGTG TACAAACCTT 1740

GAAATTAAAC AAGAAGACCC CACAAATGTG GGCCTGAAG TAAAGCAACA AGTAACCATG 1800

GTTTCAGACA CTGAAATCTT AAAGGTTGCT AGAACACATC ACGTCCAAGC AGAAAGCTAC 1860

CTGGTGTACA ACATCATGAG CAGTGGAGAG ATTGAATGCA GCAACACCCT AGAAGATGAG 1920

CTTGACCAGG CCTTACCCAG CCAGGCCTTC ATTTACCGTC CCATTCGACA GCGGGTCTAC 1980

TCACTCTTAC TGGAGGACTG TCAAGATGTC ACCAGCACCT GCCTAGCTGT CAAGGAGTGG 2040

TTTGTGTATC CTGGGAACCC ACTGAGGCAC CCGGACCTCG TCAGGCCGCT GCAGATGACC 2100

ATTCCAGGGG GAACGCCTAG TTTGAAAATA TTATGGCTGA ACCAAGAGCC AGAAATACAG 2160

GTTCGGCGCT TGGACACACT CCTAGCCTGT TTCAATCTTT CCTCCTCAAG AGAAGAGCTG 2220

CAGGCTGTCTG AAAGCCCATT TCAAGCTTTG TGCTGCCTCT TGATCTACCT CTTTGTCCAG 2280

GTGGACACGC TTTGCCTGGA GGATTTGCAT GCGTTTATTG CGCAGGCCTT GTGCCTCCAA 2340
 GGAAAATCCA CCTCGCAGCT TGTAATCTA CAGCCTGATT ACATCAACCC CAGAGCCGTG 2400
 CAGCTGGGCT CCCTTCTCGT CCGCGGCCCTC ACCACTCTGG TTTTAGTCAA CAGCGCATGT 2460
 GGCTTCCCCT GGAAGACGAG TGATTTTCATG CCCTGGAATG TATTTGACGG GAAGCTTTTT 2520
 CATCAGAAGT ACTTGCAATC TGAAAAGGGT TATGCTGTGG AGGTTCTTTT AGAACAAAAT 2580
 GGAGGTGGGG AAGACAGGGC TCCAGCTACC ACAGGACGGG CTCTGGGTAT AGCCGTTCCA 2640
 GTCAGGGACA GCCGTGGAGA GACCAGGGAC CAGGAAGCAG ACAGTATGAG CATGACCAGT 2700
 GGAGAAGGTA CTAGTCAACC TCCAGAAAGA GTATGGAGAG AAAAAGAGGC ACACCTGGAC 2760
 GCAGAGCCCT GCCAGCGCCC TCCTCTGCTG TTGCAGCTGC AAGGAGACCA TGCCTGTGGG 2820
 AGCCAGGCCT CGCTTGCATG AAGAAGGAAC GATGCCTTTT TCAATGGTGT CTCCCTCCCA 2880
 TTGTGCAGAA GAGCTTTTGT TGGCTTCTCT CCCGAGCTTG TGCCTGATTC TGTGGCCCAA 2940
 AACAATCATT GTTAACATCT TCATGTGTTT CATTCTGATC TTTCATTCAT ATATATGATG 3000
 CCTAGCTAAT TTCATTTTAA AATAAATGGG AATCTGTTGT AAAAAAAAAA AAAAAAAAAA 3060
 AAAAAAA 3067

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 916 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Val | Arg | Gly | Leu | Gln | Gly | Phe | Val | Gly | Ser | Thr | Cys | Pro | His |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Ile | Cys | Thr | Val | Val | Asn | Phe | Lys | Glu | Leu | Ala | Glu | His | His | Arg | Ser |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Lys | Tyr | Pro | Gly | Cys | Thr | Pro | Thr | Ile | Val | Val | Asp | Ala | Met | Cys | Cys |
| | | 35 | | | | | 40 | | | | 45 | | | | |
| Leu | Arg | Tyr | Trp | Tyr | Thr | Pro | Glu | Ser | Trp | Ile | Cys | Gly | Gly | Gln | Trp |
| | 50 | | | | | 55 | | | | 60 | | | | | |
| Arg | Glu | Tyr | Phe | Ser | Ala | Leu | Arg | Asp | Phe | Val | Lys | Thr | Phe | Thr | Ala |
| 65 | | | | | 70 | | | | 75 | | | | | | 80 |

Ala Gly Ile Lys Leu Ile Phe Phe Phe Asp Gly Met Val Glu Gln Asp
85 90 95

Lys Arg Asp Glu Trp Val Lys Arg Arg Leu Lys Asn Asn Arg Glu Ile
100 105 110

Ser Arg Ile Phe His Tyr Ile Lys Ser His Lys Glu Gln Pro Gly Arg
115 120 125

Asn Met Phe Phe Ile Pro Ser Gly Leu Ala Val Phe Thr Arg Phe Ala
130 135 140

Leu Lys Thr Leu Gly Gln Glu Thr Leu Cys Ser Leu Gln Glu Ala Asp
145 150 155 160

Tyr Glu Val Ala Ser Tyr Gly Leu Gln His Asn Cys Leu Gly Ile Leu
165 170 175

Gly Glu Asp Thr Asp Tyr Leu Ile Tyr Asp Thr Cys Pro Tyr Phe Ser
180 185 190

Ile Ser Glu Leu Cys Leu Glu Ser Leu Asp Thr Val Met Leu Cys Arg
195 200 205

Glu Lys Leu Cys Glu Ser Leu Gly Leu Cys Val Ala Asp Leu Pro Leu
210 215 220

Leu Ala Cys Leu Leu Gly Asp Asp Ile Ile Pro Glu Gly Met Phe Glu
225 230 235 240

Ser Phe Arg Tyr Lys Cys Leu Ser Ser Tyr Thr Ser Val Lys Glu Asn
245 250 255

Phe Asp Lys Lys Gly Asn Ile Ile Leu Ala Val Ser Asp His Ile Ser
260 265 270

Lys Val Leu Tyr Leu Tyr Gln Gly Glu Lys Lys Leu Glu Glu Ile Leu
275 280 285

Pro Leu Gly Pro Asn Lys Ala Leu Phe Tyr Lys Gly Met Ala Ser Tyr
290 295 300

Leu Leu Pro Gly Gln Lys Ser Pro Trp Phe Phe Gln Lys Pro Lys Gly
305 310 315 320

Val Ile Thr Leu Asp Lys Gln Val Ile Ser Thr Ser Ser Asp Ala Glu
325 330 335

Ser Arg Glu Glu Val Pro Met Cys Ser Asp Ala Glu Ser Arg Gln Glu
340 345 350

Val Pro Met Cys Thr Gly Pro Glu Ser Arg Arg Glu Val Pro Val Tyr
355 360 365

Thr Asp Ser Glu Pro Arg Gln Glu Val Pro Met Cys Ser Asp Pro Glu
370 375 380

Pro Arg Gln Glu Val Pro Thr Cys Thr Gly Pro Glu Ser Arg Arg Glu
385 390 395 400

Val Pro Met Cys Ser Asp Pro Glu Pro Arg Gln Glu Val Pro Met Cys
405 410 415

Thr Gly Pro Glu Ala Arg Gln Glu Val Pro Met Tyr Thr Asp Ser Glu
420 425 430

Pro Arg Gln Glu Val Pro Met Tyr Thr Asp Ser Glu Pro Arg Gln Glu
435 440 445

Val Pro Met Tyr Thr Gly Ser Glu Pro Arg Gln Glu Val Pro Met Tyr
450 455 460

Thr Gly Pro Glu Ser Arg Gln Glu Val Pro Met Tyr Thr Gly Pro Glu
465 470 475 480

Ser Arg Gln Glu Val Leu Ile Arg Thr Asp Pro Glu Ser Arg Gln Glu
485 490 495

Ile Met Cys Thr Gly His Glu Ser Lys Gln Glu Val Pro Ile Cys Thr
500 505 510

Asp Pro Ile Ser Lys Gln Glu Asp Ser Met Cys Thr His Ala Glu Ile
515 520 525

Asn Gln Lys Leu Pro Val Ala Thr Asp Phe Glu Phe Lys Leu Glu Ala
530 535 540

Leu Met Cys Thr Asn Pro Glu Ile Lys Gln Glu Asp Pro Thr Asn Val
545 550 555 560

Gly Pro Glu Val Lys Gln Gln Val Thr Met Val Ser Asp Thr Glu Ile
565 570 575

Leu Lys Val Ala Arg Thr His His Val Gln Ala Glu Ser Tyr Leu Val
580 585 590

Tyr Asn Ile Met Ser Ser Gly Glu Ile Glu Cys Ser Asn Thr Leu Glu
595 600 605

Asp Glu Leu Asp Gln Ala Leu Pro Ser Gln Ala Phe Ile Tyr Arg Pro
610 615 620

Ile Arg Gln Arg Val Tyr Ser Leu Leu Leu Glu Asp Cys Gln Asp Val
625 630 635 640

Thr Ser Thr Cys Leu Ala Val Lys Glu Trp Phe Val Tyr Pro Gly Asn
645 650 655

Pro Leu Arg His Pro Asp Leu Val Arg Pro Leu Gln Met Thr Ile Pro
660 665 670

Gly Gly Thr Pro Ser Leu Lys Ile Leu Trp Leu Asn Gln Glu Pro Glu
675 680 685

Ile Gln Val Arg Arg Leu Asp Thr Leu Leu Ala Cys Phe Asn Leu Ser
690 695 700

Ser Ser Arg Glu Glu Leu Gln Ala Val Glu Ser Pro Phe Gln Ala Leu
705 710 715 720

Cys Cys Leu Leu Ile Tyr Leu Phe Val Gln Val Asp Thr Leu Cys Leu
725 730 735

Glu Asp Leu His Ala Phe Ile Ala Gln Ala Leu Cys Leu Gln Gly Lys
740 745 750

Ser Thr Ser Gln Leu Val Asn Leu Gln Pro Asp Tyr Ile Asn Pro Arg
755 760 765

Ala Val Gln Leu Gly Ser Leu Leu Val Arg Gly Leu Thr Thr Leu Val
770 775 780

Leu Val Asn Ser Ala Cys Gly Phe Pro Trp Lys Thr Ser Asp Phe Met
785 790 795 800

Pro Trp Asn Val Phe Asp Gly Lys Leu Phe His Gln Lys Tyr Leu Gln
805 810 815

Ser Glu Lys Gly Tyr Ala Val Glu Val Leu Leu Glu Gln Asn Gly Gly
820 825 830

Gly Glu Asp Arg Ala Pro Ala Thr Thr Gly Arg Ala Leu Gly Ile Ala
835 840 845

Val Pro Val Arg Asp Ser Arg Gly Glu Thr Arg Asp Gln Glu Ala Asp
850 855 860

Ser Met Ser Met Thr Ser Gly Glu Gly Thr Ser Gln Pro Pro Glu Arg
865 870 875 880

Val Trp Arg Glu Lys Glu Ala His Leu Asp Ala Glu Pro Cys Gln Arg
885 890 895

Pro Pro Leu Leu Leu Gln Leu Gln Gly Asp His Ala Cys Gly Ser Gln
900 905 910

Ala Ser Leu Ala
915

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1914 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

| | |
|--|------|
| AGCTGTCTGC TCTCCTGGCA GGAATCGCTG AGGGAGGGAA ACGCGGCTCT GAATCAGCCC | 60 |
| AGAACGAGCC TTCGGGAAGC TCACCCTCCG ATCTCGGTGT GATTGTTGTG ATTGTTGTGA | 120 |
| TTTCCTGTCT CGTTTGCCTT GACCGCCATG TGAAAGAATC TGTTCCCCAG CTAGGTGGGG | 180 |
| AAAATTACACA GGTGGGCTGT CTGTAGAGAG AACTGGCTGA TTAAAGGCTT CTCGTCCCGA | 240 |
| TTTTGTGATA GCCAAGTGCT TGGCCTGGTC GACGGTCTTT GCTCCTTTAC AAATAAAGTG | 300 |
| TTCTGTTTCA GTTCGTCCCA AGTTTTCCAT GAAGGGCAGT GGTTCCTTGA CCTCCCAGGT | 360 |
| GCCTGGGCTT CCCCAGGTTT CTGATCTGGG GCTTGGGGCC CTGTGTTTGG GGATCGTGGC | 420 |
| ACTGTGTGCA CCAGCCTGGA AGCACTGGGC CAGTCTTGGC CAAGCTTTCC ATCAGGGATG | 480 |
| ATTTGATCTT GGTGCTACAG GTCTGTGGTA CGACCATTGT TCCACACCAC ATGTCATTAA | 540 |
| TAATGCTTCC CATGCTTCTG CTTGCAAATG ACCAGCCTTC CAAACAGCCA GAGCTGTTTC | 600 |
| GAGGTGTTTC TGCAGGCAGG TGCAGGCGTG CCCTCAAATA AGCTTTGCCA ATGGAGTCTC | 660 |
| AGCAAGAGCA AAACCTGGTC AGGAAAGACA AAGCCTGGGA ATCCACCCCC ATGCCCTGCA | 720 |
| GGTTGGCTGG CCCTGGAGCC ATTTATTATA GTGCTAATCA TGTTTCTAGG CAGGTGCAGA | 780 |
| TGGCAAGGGC AGTGTCTTGG TGAGCTTTTT AGCACGAAGA GCCAGGTCTG TCGAAGCCTT | 840 |
| TGTGAGAGCT GGAAACGCAG GTGTGCTGGG CATGCGCAGT ATGGGGTTTC GGGCTCAGGG | 900 |
| CTTGCCCTTT GGCATCAGAC AGACCTGGCT TCGCATCCTG GATTGCTTC TGACGTGCAC | 960 |
| CCTTCCCTTT GGGTCTCGTG ATGTGAAATG GAGATGTTGT CATTTGTGAG GGCTCCATGA | 1020 |
| AGTTTCGTTG AAATGACAAA TACTAATTTT TTCATCTGTG AAATGGAGAT AATAGTGCTG | 1080 |
| ACCTCAGAAC AGCTGAGAGG ACTAAATGAA ATGATGTTGG ATGTAGCCAT AAAGAACGAA | 1140 |
| GTCAGGCACT GGTGCACGCC TGGAATCCCA GCTCTTGGGA GACCGAGACA GGTGGATTGC | 1200 |
| TTGAGCTCAG GAGTTTGAGA CCAGCCTGAG CAACATAGGG AGGTCCAGTC TCTACAAAAA | 1260 |
| ATATGAAAAG TAGCTGGGCG TGGTGGCGCA TGCCTGTAGT CCCACTACTT GGAAGGCTTC | 1320 |
| GTTGGGAGGA TCACTTGAGC CCAGAAGATT GAGGCTGCAG TAAGCCGTGA TCGTGCCACT | 1380 |
| GCATTCCAGC CTGGGCAACA GAGCGAGACA CTGTCTCAAA TAAAAAAGAT GGGGAATAGTA | 1440 |
| GACACTGGGG GCTCCAGAAG GAGGGAGGGA GGGAGGAAGG GGAGGAAGGG CTGAAATGCT | 1500 |
| TTCTATTGGA TACTATCTGG GCATATTACT TCCTGTGGTT CACTGTC'TGG GTGACAGGAT | 1560 |
| TCATAGAAGC CCAAAC'TTTA GCACCACGCA GCATACCCTT GTAACAAAGC CGCACACGTA | 1620 |
| CGCCCTCAAG CTAAAACAAA AGTGGACCGG GAGGCCGAGG TCGGGGGATC ATGAGGTCAG | 1680 |

GAGTTTGAGA CCAGCCTGGC AGATAACGGT GAAACCCCGT CTCTACTAAA AATACCAAAA 1740
 AAAGTTAGCC GGACATGGTG GCAGGTGCCT GTAGTCCCAG CTACTTGGGA GGCTGGGGCA 1800
 GAAGAATCGC TTGAACCCAG GAGGCGGAGG TTGCAGTGAG CCGAGATTGC GCCACTGCAC 1860
 TCCAGCCTGT GCGACAGAGT GAGACTCCGT CTCAAAAAAA AAAAAAAAAA AAAA 1914

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Thr | Ser | Leu | Pro | Asn | Ser | Gln | Ser | Cys | Phe | Glu | Val | Phe | Leu | Gln | 1 | 5 | 10 | 15 |
| Ala | Gly | Ala | Gly | Val | Pro | Ser | Asn | Lys | Leu | Cys | Gln | Trp | Ser | Leu | Ser | 20 | 25 | 30 | |
| Lys | Ser | Lys | Thr | Trp | Ser | Gly | Lys | Thr | Lys | Pro | Gly | Asn | Pro | Pro | Pro | 35 | 40 | 45 | |
| Cys | Pro | Ala | Gly | Trp | Leu | Ala | Leu | Glu | Pro | Phe | Ile | Ile | Val | Leu | Ile | 50 | 55 | 60 | |
| Met | Phe | Leu | Gly | Arg | Cys | Arg | Trp | Gln | Gly | Gln | Cys | Leu | Gly | Glu | Leu | 65 | 70 | 75 | 80 |
| Phe | Ser | Thr | Lys | Ser | Gln | Val | Cys | Arg | Ser | Leu | Cys | Glu | Ser | Trp | Lys | 85 | 90 | 95 | |
| Arg | Arg | Cys | Ala | Gly | His | Ala | Gln | Tyr | Gly | Val | Ser | Gly | Ser | Gly | Leu | 100 | 105 | 110 | |
| Ala | Leu | Trp | His | Gln | Thr | Asp | Leu | Ala | Ser | His | Pro | Gly | Phe | Ala | Ser | 115 | 120 | 125 | |
| Asp | Val | His | Pro | Ser | Leu | Trp | Val | Ser | 130 | 135 | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 575 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

```

CCGACTCCCT TCTTTATGGC GTCGCTCCTG TGCTGTGGGC CGAAGCTGGC CGCCTGCGGC      60
ATCGTCCTCA GCGCCTGGGG AGTGATCATG TTGATAATGC TCGGAATATT TTTCAATGTC      120
CATTCCGCTG TGTTGATTGA GGACGTTCCC TTCACGGAGA AAGATTTTGA GAATGGCCCC      180
CAGAACATAT ACAACCTTTA CGAGCAAGTC AGCTACAAC TTTTCATCGC TGCAGGCCTT      240
TACCTCCTCC TCGGAGGCTT CTCTTTCTGC CAAGTTCGGC TCAATAAGCG CAAGGAATAC      300
ATGGTGCGCT AGGGCCCCGG CGCGTTTCCC CGCTCCAGCC CCTCCTCTAT TTAAAGACTC      360
CCTGCACCGT GTCACCCAGG TCGCGTCCCA CCCTTGCCGG CGCCCTCTGT GGGACTGGGT      420
TTCCCGGGCG AGAGACTGAA TCCCTTCTCC CATCTCTGGC ATCCGGCCCC CGTGGAGAGG      480
GCTGAGGCTG GGGGGCTGTT CCGTCTCTCC ACCCTTCGCT GTGTCCCGTA TCTCAATAAA      540
GAGAATCTGC TCTCTTCAA AAAAAAAAAA AAAAAA      575

```

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 98 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```

Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu Ala Ala Cys Gly Ile
1           5           10          15
Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile Met Leu Gly Ile Phe
20          25          30
Phe Asn Val His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr Glu
35          40          45
Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Glu Gln
50          55          60
Val Ser Tyr Asn Cys Phe Ile Ala Ala Gly Leu Tyr Leu Leu Leu Gly
65          70          75          80
Gly Phe Ser Phe Cys Gln Val Arg Leu Asn Lys Arg Lys Glu Tyr Met

```


85

90

95

Val Arg

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GNAGCCCAGGA GTCTTCTCAA CCTCTTCC

29

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ANCAGTCGCAA GTGCATAGTA ACCCAGTA

29

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TNCTCAGCTTT TATTTGGTTC TGAGTGTT

29

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TNTGCTCAGAC CAGTCATCTG CAGAATCA

29

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

TNCAGCACTGT CTTAGGCTAA ATTTCCCA

29

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GNATTCGGCGT CTGAACTCGT GGATATTA

29

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

ANATGCCCAGA TAGTATCCAA TAGAAAGC

29

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

CNACAGCACAG GAGCGACGCC ATAAAGAA

29

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 543 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Met Val Met Tyr Ala Arg Lys Gln Gln Arg Leu Ser Asp Gly Cys His
1 5 10 15

Asp Arg Arg Gly Asp Ser Gln Pro Tyr Gln Ala Leu Lys Tyr Ser Ser
20 25 30

Lys Ser His Pro Ser Ser Gly Asp His Arg His Glu Lys Met Arg Asp
35 40 45

Ala Gly Asp Pro Ser Pro Pro Asn Lys Met Leu Arg Arg Ser Asp Ser
50 55 60

Pro Glu Asn Lys Tyr Ser Asp Ser Thr Gly His Ser Lys Ala Lys Asn
65 70 75 80

Val His Thr His Arg Val Arg Glu Arg Asp Gly Gly Thr Ser Tyr Ser
85 90 95

Pro Gln Glu Asn Ser His Asn His Ser Ala Leu His Ser Ser Asn Ser
100 105 110

His Ser Ser Asn Pro Ser Asn Asn Pro Ser Lys Thr Ser Asp Ala Pro
115 120 125

Tyr Asp Ser Ala Asp Asp Trp Ser Glu His Ile Ser Ser Ser Gly Lys
130 135 140

Lys Tyr Tyr Tyr Asn Cys Arg Thr Glu Val Ser Gln Trp Glu Lys Pro
145 150 155 160

Lys Glu Trp Leu Glu Arg Glu Gln Arg Gln Lys Glu Ala Asn Lys Met
165 170 175

Ala Val Asn Ser Phe Pro Lys Asp Arg Asp Tyr Arg Arg Glu Val Met
180 185 190

Gln Ala Thr Ala Thr Ser Gly Phe Ala Ser Gly Lys Ser Thr Ser Gly
195 200 205

Asp Lys Pro Val Ser His Ser Cys Thr Thr Pro Ser Thr Ser Ser Ala
210 215 220

Ser Gly Leu Asn Pro Thr Ser Ala Pro Pro Thr Ser Ala Ser Ala Val
225 230 235 240

Pro Val Ser Pro Val Pro Gln Ser Pro Ile Pro Pro Leu Leu Gln Asp
245 250 255

Pro Asn Leu Leu Arg Gln Leu Leu Pro Ala Leu Gln Ala Thr Leu Gln
260 265 270

Leu Asn Asn Ser Asn Val Asp Ile Ser Lys Ile Asn Glu Val Leu Thr
275 280 285

Ala Ala Val Thr Gln Ala Ser Leu Gln Ser Ile Ile His Lys Phe Leu
290 295 300

Thr Ala Gly Pro Ser Ala Phe Asn Ile Thr Ser Leu Ile Ser Gln Ala
305 310 315 320

Ala Gln Leu Ser Thr Gln Ala Gln Pro Ser Asn Gln Ser Pro Met Ser
325 330 335

Leu Thr Ser Asp Ala Ser Ser Pro Arg Ser Tyr Val Ser Pro Arg Ile
340 345 350

Ser Thr Pro Gln Thr Asn Thr Val Pro Ile Lys Pro Leu Ile Ser Thr
355 360 365

Pro Pro Val Ser Ser Gln Pro Lys Val Ser Thr Pro Val Val Lys Gln
370 375 380

Gly Pro Val Ser Gln Ser Ala Thr Gln Gln Pro Val Thr Ala Asp Lys
385 390 395 400

Gln Gln Gly His Glu Pro Val Ser Pro Arg Ser Leu Gln Arg Ser Ser

| | | |
|---|-----|-----|
| 405 | 410 | 415 |
| Gln Arg Ser Pro Ser Pro Gly Pro Asn His Thr Ser Asn Ser Ser Asn | | |
| 420 | 425 | 430 |
| Ala Ser Asn Ala Thr Val Val Pro Gln Asn Ser Ser Ala Arg Ser Thr | | |
| 435 | 440 | 445 |
| Cys Ser Leu Thr Pro Ala Leu Ala Ala His Phe Ser Glu Asn Leu Ile | | |
| 450 | 455 | 460 |
| Lys His Val Gln Gly Trp Pro Ala Asp His Ala Glu Lys Gln Ala Ser | | |
| 465 | 470 | 475 |
| Arg Leu Arg Glu Glu Ala His Asn Met Gly Thr Ile His Met Ser Glu | | |
| 485 | 490 | 495 |
| Ile Cys Thr Glu Leu Lys Asn Leu Arg Ser Leu Val Arg Val Cys Glu | | |
| 500 | 505 | 510 |
| Ile Gln Ala Thr Leu Arg Glu Gln Arg Ile Leu Phe Leu Arg Gln Gln | | |
| 515 | 520 | 525 |
| Ile Lys Glu Leu Glu Lys Leu Lys Asn Gln Asn Ser Phe Met Val | | |
| 530 | 535 | 540 |

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1755 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

| | |
|---|-----|
| CAGTGGAGTC TGTACTGGCT GCGGGGGACC CTGCTCATTT GAAAATCTGA CATCAGCTGG | 60 |
| GCAGTCGCCC CCCTCCTCCT TTCCTCCCTC TACTCTGACA CAGCACTTAG CACCTGAATC | 120 |
| TTCGTTTCTC TCCCAGGGAC CCTCCATTTT CCATATCCAG GAAAATGTGA TGCGCCACAG | 180 |
| GTATCAGCGT CTGGATCGCC ACTTCACGTT TTAGCCACAA GTGACTCAGT GGAAGATCCA | 240 |
| GAGTCAACAG AGGCTCGTCA GGAAGATGTC TACAGAAAAG GTAGACCAAA AGGAGGAAGC | 300 |
| TGGGGAAAAA GAGGTGTGCG GAGACCAGAT CAARGGACCG GACAAAGAGG AGGAACCACC | 360 |
| AGCTGCTGCA TCCCATGGCC AGGGGTGGCG TCCAGGTGGC AGAGCAGCTA GGAACGCAAG | 420 |
| GCCTGAACCT GGGGCCAGAC ACCCTGCTCT CCCGGCCATG GTCAACGACC CTCCAGTACC | 480 |
| TGCCTTACTG TGGGCCCAGG AGGTGGGCCA AGTCTTGGCA GGCCGTGCCC GCAGGCTGCT | 540 |

| | |
|---|------|
| GCTGCAGTTT GGGGTGCTCT TCTGCACCAT CCTCCTTTTG CTCTGGGTGT CTGTCTTCCT | 600 |
| CTATGGCTCC TTCTACTATT CCTATATGCC GACAGTCAGC CACCTCAGCC CTGTGCATTT | 660 |
| CTACTACAGG ACCGACTGTG ATTCCTCCAC CACCTCACTC TGCTCCTTCC CTGTTGCCAA | 720 |
| TGTCTCGCTG ACTAAGGGTG GACGTGATCG GGTGCTGATG TATGGACAGC CGTATCGTGT | 780 |
| TACCTTAGAG CTTGAGCTGC CAGAGTCCCC TGTGAATCAA GATTTGGGCA TGTTCCTGGT | 840 |
| CACCATTTC TGCTACACCA GAGGTGGCCG AATCATCTCC ACTTCTTCGC GTTCGGTGAT | 900 |
| GCTGCATTAC CGCTCAGACC TGCTCCAGAT GCTGGACACA CTGGTCTTCT CTAGCCTCCT | 960 |
| GCTATTTGGC TTTGCAGAGC AGAAGCAGCT GCTGGAGGTG GAACTCTACG CAGACTATAG | 1020 |
| AGAGAACTCG TACGTGCCGA CCACTGGAGC GATCATTGAG ATCCACAGCA AGCGCATCCA | 1080 |
| GCTGTATGGA GCCTACCTCC GCATCCACGC GCACTTCACT GGGCTCAGAT ACCTGCTATA | 1140 |
| CAACTTCCCG ATGACCTGCG CCTTCATAGG TGTGCCAGC AACTTCACCT TCCTCAGCGT | 1200 |
| CATCGTGCTC TTCAGCTACA TGCAGTGGGT GTGGGGGGGC ATCTGGCCCC GACACCGCTT | 1260 |
| CTCTTTGCAG GTTAACATCC GAAAAAGAGA CAATTCCCGG AAGGAAGTCC AACGAAGGAT | 1320 |
| CTCTGCTCAT CAGCCAGGGC CTGAAGGCCA GGAGGAGTCA ACTCCGCAAT CAGATGTTAC | 1380 |
| AGAGGATGGT GAGAGCCCTG AAGATCCCTC AGGGACAGAG GGTCAGCTGT CCGAGGAGGA | 1440 |
| GAAACCAGAT CAGCAGCCCC TGAGCGGAGA AGAGGAGCTA GAGCCTGAGG CCAGTGATGG | 1500 |
| TTCAGGCTCC TGGGAAGATG CAGCTTTGCT GACGGAGGCC AACCTGCCTG CTCCTGCTCC | 1560 |
| TGCTTCTGCT TCTGCCCCTG TCCTAGAGAC TCTGGGCAGC TCTGAACCTG CTGGGGGTGC | 1620 |
| TCTCCGACAG CGCCCCACCT GCTCTAGTTC CTGAAGAAAA GGGGCAGACT CCTCACATTC | 1680 |
| CAGCACTTTC CCACCTGACT CCTCTCCCCT CGTTTTTCCT TCAATAAACT ATTTTGTGTC | 1740 |
| AAAAAAAAAA AAAAA | 1755 |

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Thr | Glu | Lys | Val | Asp | Gln | Lys | Glu | Glu | Ala | Gly | Glu | Lys | Glu | 1 | 5 | 10 | 15 |
| Val | Cys | Gly | Asp | Gln | Ile | Lys | Gly | Pro | Asp | Lys | Glu | Glu | Glu | Pro | Pro | 20 | 25 | 30 | |
| Ala | Ala | Ala | Ser | His | Gly | Gln | Gly | Trp | Arg | Pro | Gly | Gly | Arg | Ala | Ala | 35 | 40 | 45 | |
| Arg | Asn | Ala | Arg | Pro | Glu | Pro | Gly | Ala | Arg | His | Pro | Ala | Leu | Pro | Ala | 50 | 55 | 60 | |
| Met | Val | Asn | Asp | Pro | Pro | Val | Pro | Ala | Leu | Leu | Trp | Ala | Gln | Glu | Val | 65 | 70 | 75 | 80 |
| Gly | Gln | Val | Leu | Ala | Gly | Arg | Ala | Arg | Arg | Leu | Leu | Leu | Gln | Phe | Gly | 85 | 90 | 95 | |
| Val | Leu | Phe | Cys | Thr | Ile | Leu | Leu | Leu | Leu | Trp | Val | Ser | Val | Phe | Leu | 100 | 105 | 110 | |
| Tyr | Gly | Ser | Phe | Tyr | Tyr | Ser | Tyr | Met | Pro | Thr | Val | Ser | His | Leu | Ser | 115 | 120 | 125 | |
| Pro | Val | His | Phe | Tyr | Tyr | Arg | Thr | Asp | Cys | Asp | Ser | Ser | Thr | Thr | Ser | 130 | 135 | 140 | |
| Leu | Cys | Ser | Phe | Pro | Val | Ala | Asn | Val | Ser | Leu | Thr | Lys | Gly | Gly | Arg | 145 | 150 | 155 | 160 |
| Asp | Arg | Val | Leu | Met | Tyr | Gly | Gln | Pro | Tyr | Arg | Val | Thr | Leu | Glu | Leu | 165 | 170 | 175 | |
| Glu | Leu | Pro | Glu | Ser | Pro | Val | Asn | Gln | Asp | Leu | Gly | Met | Phe | Leu | Val | 180 | 185 | 190 | |
| Thr | Ile | Ser | Cys | Tyr | Thr | Arg | Gly | Gly | Arg | Ile | Ile | Ser | Thr | Ser | Ser | 195 | 200 | 205 | |
| Arg | Ser | Val | Met | Leu | His | Tyr | Arg | Ser | Asp | Leu | Leu | Gln | Met | Leu | Asp | 210 | 215 | 220 | |
| Thr | Leu | Val | Phe | Ser | Ser | Leu | Leu | Leu | Phe | Gly | Phe | Ala | Glu | Gln | Lys | 225 | 230 | 235 | 240 |
| Gln | Leu | Leu | Glu | Val | Glu | Leu | Tyr | Ala | Asp | Tyr | Arg | Glu | Asn | Ser | Tyr | 245 | 250 | 255 | |
| Val | Pro | Thr | Thr | Gly | Ala | Ile | Ile | Glu | Ile | His | Ser | Lys | Arg | Ile | Gln | 260 | 265 | 270 | |
| Leu | Tyr | Gly | Ala | Tyr | Leu | Arg | Ile | His | Ala | His | Phe | Thr | Gly | Leu | Arg | 275 | 280 | 285 | |
| Tyr | Leu | Leu | Tyr | Asn | Phe | Pro | Met | Thr | Cys | Ala | Phe | Ile | Gly | Val | Ala | 290 | 295 | 300 | |

Ser Asn Phe Thr Phe Leu Ser Val Ile Val Leu Phe Ser Tyr Met Gln
305 310 315 320

Trp Val Trp Gly Gly Ile Trp Pro Arg His Arg Phe Ser Leu Gln Val
325 330 335

Asn Ile Arg Lys Arg Asp Asn Ser Arg Lys Glu Val Gln Arg Arg Ile
340 345 350

Ser Ala His Gln Pro Gly Pro Glu Gly Gln Glu Glu Ser Thr Pro Gln
355 360 365

Ser Asp Val Thr Glu Asp Gly Glu Ser Pro Glu Asp Pro Ser Gly Thr
370 375 380

Glu Gly Gln Leu Ser Glu Glu Glu Lys Pro Asp Gln Gln Pro Leu Ser
385 390 395 400

Gly Glu Glu Glu Leu Glu Pro Glu Ala Ser Asp Gly Ser Gly Ser Trp
405 410 415

Glu Asp Ala Ala Leu Leu Thr Glu Ala Asn Leu Pro Ala Pro Ala Pro
420 425 430

Ala Ser Ala Ser Ala Pro Val Leu Glu Thr Leu Gly Ser Ser Glu Pro
435 440 445

Ala Gly Gly Ala Leu Arg Gln Arg Pro Thr Cys Ser Ser Ser
450 455 460

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

| | |
|--|-----|
| GGAATAGAGG ATTTCAAAAA GCATGCGTTT TTTGAAGGTC TAAATTGGGA AAATATACGA | 60 |
| AACCTAGAAG CACCTTATAT TCCTGATGTG AGCAGTCCCT CTGACACATC CAACTTCGAC | 120 |
| GTGGATGACG ACGTGCTGAG AAACACGGAA ATATTACCTC CTGGTTCTCA CACAGGCTTT | 180 |
| TCTGGATTAC ATTTGCCATT CATTGGTTTT ACATTCACAA CGGAAAGCTG TTTTCTGAT | 240 |
| CGAGGCTCTC TGAAGAGCAT AATGCAGTCC AACACATTAA CCAAAGATGA GGATGTGCAG | 300 |
| CGGGACCTGG AGCACAGCCT GCAGATGGAA GCTTACGAGA GGAGGATTCTG GAGGCTGGAA | 360 |
| CAGGAGAAGC TGGAGCTGAG CAGGAAGCTG CAAGAGTCCA CCCAGACCGT GCAGTCCCTC | 420 |

| | | | | | | |
|-------------|------------|-------------|------------|------------|-------------|------|
| CACGGCTCAT | CTCGGGCCCT | CAGCAATTCA | AACCGAGATA | AAGAAATCAA | AAAGCTAAAT | 480 |
| GAAGAAATCG | AACGCTTGAA | GAATAAAATA | GCAGATTCAA | ACAGGCTGGA | GCGACAGCTT | 540 |
| GAGGACACAG | TGGCGCTTCG | CCAAGAGCGT | GAGGACTCCA | CGCAGCGGCT | GCGGGGGCTG | 600 |
| GAGAAGCAGC | ACCGCGTGGT | CCGGCAGGAG | AAGGAGGAGC | TGCACAAGCA | ACTGGTTGAA | 660 |
| GCCTCAGAGC | GGTTGAAATC | CCAGGCCAAG | GAACTCAAAG | ATGCCCATCA | GCAGCGAAAAG | 720 |
| CTGGCCCTGC | AGGAGTTCTC | GGAGCTGAAC | GAGCGCATGG | CAGAGCTCCG | TGCCCAGAAG | 780 |
| CAGAAGGTGT | CCCGGCAGCT | GCGAGACAAG | GAGGAGGAGA | TGGAGGTGGC | CACGCAGAAG | 840 |
| GTGGACGCCA | TGCGGCAGGA | AATGCGGAGA | GCTGAGAAGC | TCAGGAAAGA | GCTGGAAGCT | 900 |
| CAGCTTGATG | ATGCTGTTGC | TGAGGCCTCC | AAGGAGCGCA | AGCTTCGTGA | GCACAGCGAG | 960 |
| AACTTCTGCA | AGCAAATGGA | AAGCGAGCTG | GAGGCCCTCA | AGGTGAAGCA | AGGAGGCCCG | 1020 |
| GGAGCGGGTG | CCACCTTAGA | GCACCAGCAA | GAGATTTCCT | AAATCAAATC | CGAGCTGGAG | 1080 |
| AAGAAAGTCT | TATTTTATGA | AGAGGAATTG | GTCAGACGTG | AGGCCTCCCA | TGTGCTAGAA | 1140 |
| GTGAAAAATG | TGAAGAAGGA | GGTGCATGAT | TCAGAAAGCC | ACCAGCTGGC | CCTGCAGAAA | 1200 |
| GAAATCTTGA | TGTTAAAAGA | TAAGTTAGAA | AAGTCAAAGC | GAGAACGGCA | TAACGAGATG | 1260 |
| GAGGAGGCAG | TAGGTACAAT | AAAAGATAAA | TACGAACGAG | AAAGAGCGAT | GCTGTTTGAT | 1320 |
| GAAAACAAGA | AGCTAACTGC | TGAAAAATGAA | AAGCTCTGTT | CCTTTGTGGA | TAAACTCACA | 1380 |
| GCTCAAAAATA | GACAGCTGGA | GGATGAGCTG | CAGGATCTGG | CAGCCAAGAA | GGAGTCAGTG | 1440 |
| GCCCACTGGG | AAGCTCAGAT | TGCGGAAATC | ATTCACTGGG | TCAGTGACGA | GAAAGATGCC | 1500 |
| CGGGGTTACC | TTCAAGCTCT | TGCTTCCAAG | ATGACCGAAG | AGCTCGAGGC | TTTGAGGAGT | 1560 |
| TCTAGTCTGG | GGTCAAGAAC | ACTGGACCCG | CTGTGGAAGG | TGCGCCGCAG | CCAGAAGCTG | 1620 |
| GACATGTCCG | CGCGGCTGGA | GCTGCAGTCG | GCCCTGGAGG | CGGAGATCCG | GGCCAAGCAG | 1680 |
| CTTGTCAGG | AGGAGCTCAG | GAAGGTCAAG | GACGCCAACC | TCACCTTGGA | AAGCAAACYA | 1740 |
| AWGGATTCCG | AAGCCAAAAA | CAGAGAATTA | TTAGAAGAAA | TGGAAATTTT | GAAGAAAAAG | 1800 |
| ATGGAAGAAA | AATTCAGAGC | AGATACTGGG | CTCAAACCTC | CAGATTTTCA | GGATTCCATT | 1860 |
| TTTGAGTATT | TCAACACTGC | TCCTCTTGCA | CATGACCTGA | CATTTAGAAC | CAGCTCAGCT | 1920 |
| AGTGAGCAAG | AAACACAAGC | TCCGAAGCCA | GAAGCGTCCC | CGTCGATGTC | TGTGGCTGCA | 1980 |
| TCAGAGCAGC | AGGAGGACAT | GGCTCGGCCC | CCGCAGAGGC | CATCCGCTGT | GCCGTTGCCC | 2040 |
| ACCACGCAGG | CCCTGGCTCT | GGCTGGACCG | AAGCCAAAAG | CTCACCAGTT | CAGCATCAAG | 2100 |

TCCTTCTCCA GCCCTACTCA GTGCAGCCAC TGCACCTCCC TGATGGTTGG GCTGATCCGG 2160
CAGGGCTACG CCTGCGAGGT GTGTTCTTTT GCTTGCCACG TGTCTGCAA AGACGGTGCC 2220
CCCCAGGTGT GCCCAATACC TCCCAGACAG TCCAAGAGGC CTCTGGGCGT GGACGTGCAG 2280
CGAGGCATCG GAACAGCCTA CAAAGGCCAT GTCAAGGTCC CAAAGCCCAC GGGGGTGAAG 2340
AAGGGATGGC AGCGCGCATA TGCAGTCGTC TGTGACTGCA AGCTCTTCCT GTATGATCTG 2400
CCTGAAGGAA AATCCACCCA GCCTGGTGTC ATTGCGAGCC AAGTCTTGGA TCTCAGAGAT 2460
GACGAGTTTT CCGTGAGCTC AGTCCTGGCC TCAGATGTCA TTCATGCTAC ACGCCGAGAT 2520
ATTCCATGTA TATTCAGGGT GACGGCCTCT CTCTTAGGTG CACCTTCTAA GACCAGCTCG 2580
CTGCTCATTG TGACAGAAAA TGAGAATGAA AAGAGGAAGT GGGTTGGGAT TCTAGAAGGA 2640
CTCCAGTCCA TCCTTCATAA AAACCGGCTG AGGAATCAGG TCGTGCATGT TCCCTTGGA 2700
GCCTACGACA GCTCGCTGCC TCTCATCAAG GCCATCCTGA CAGCTGCCAT CGTGGATGCA 2760
GACAGGATTG CAGTCGGCCT AGAAGAAGGG CTCTATGTCA TAGAGGTCAC CCGAGATGTG 2820
ATCGTCCGTG CCGCTGACTG TAAGAAGGTA CACCAGATCG AGCTTGCTCC CAGGGAGAAG 2880
ATCGTAATCC TCCTCTGTGG CCGGAACCAC CATGTGCACC TCTATCCGTG GTCGTCCCTT 2940
GATGGAGCGG AAGGCAGCTT TGACATCAAG CTTCCGAAA CCAAAGGCTG CCAGCTCATG 3000
GCCACGGCCA CACTCAAGAG GARCTCTGGC ACCTGCCTGT TTGTGGCCGT GAAACGGCTG 3060
ATCCTTTGCT ATGAGATCCA GAAAATAAAG CCATATTGAA TGATAAAAAA AAAAAAAAAA 3120
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 3180
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA 3213

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 945 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Met Gln Ser Asn Thr Leu Thr Lys Asp Glu Asp Val Gln Arg Asp Leu
1 5 10 15
Glu His Ser Leu Gln Met Glu Ala Tyr Glu Arg Arg Ile Arg Arg Leu
20 25 30

Glu Gln Glu Lys Leu Glu Leu Ser Arg Lys Leu Gln Glu Ser Thr Gln
 35 40 45
 Thr Val Gln Ser Leu His Gly Ser Ser Arg Ala Leu Ser Asn Ser Asn
 50 55 60
 Arg Asp Lys Glu Ile Lys Lys Leu Asn Glu Glu Ile Glu Arg Leu Lys
 65 70 75 80
 Asn Lys Ile Ala Asp Ser Asn Arg Leu Glu Arg Gln Leu Glu Asp Thr
 85 90 95
 Val Ala Leu Arg Gln Glu Arg Glu Asp Ser Thr Gln Arg Leu Arg Gly
 100 105 110
 Leu Glu Lys Gln His Arg Val Val Arg Gln Glu Lys Glu Glu Leu His
 115 120 125
 Lys Gln Leu Val Glu Ala Ser Glu Arg Leu Lys Ser Gln Ala Lys Glu
 130 135 140
 Leu Lys Asp Ala His Gln Gln Arg Lys Leu Ala Leu Gln Glu Phe Ser
 145 150 155 160
 Glu Leu Asn Glu Arg Met Ala Glu Leu Arg Ala Gln Lys Gln Lys Val
 165 170 175
 Ser Arg Gln Leu Arg Asp Lys Glu Glu Glu Met Glu Val Ala Thr Gln
 180 185 190
 Lys Val Asp Ala Met Arg Gln Glu Met Arg Arg Ala Glu Lys Leu Arg
 195 200 205
 Lys Glu Leu Glu Ala Gln Leu Asp Asp Ala Val Ala Glu Ala Ser Lys
 210 215 220
 Glu Arg Lys Leu Arg Glu His Ser Glu Asn Phe Cys Lys Gln Met Glu
 225 230 235 240
 Ser Glu Leu Glu Ala Leu Lys Val Lys Gln Gly Gly Arg Gly Ala Gly
 245 250 255
 Ala Thr Leu Glu His Gln Gln Glu Ile Ser Lys Ile Lys Ser Glu Leu
 260 265 270
 Glu Lys Lys Val Leu Phe Tyr Glu Glu Glu Leu Val Arg Arg Glu Ala
 275 280 285
 Ser His Val Leu Glu Val Lys Asn Val Lys Lys Glu Val His Asp Ser
 290 295 300
 Glu Ser His Gln Leu Ala Leu Gln Lys Glu Ile Leu Met Leu Lys Asp
 305 310 315 320
 Lys Leu Glu Lys Ser Lys Arg Glu Arg His Asn Glu Met Glu Glu Ala
 325 330 335

Val Gly Thr Ile Lys Asp Lys Tyr Glu Arg Glu Arg Ala Met Leu Phe
340 345 350

Asp Glu Asn Lys Lys Leu Thr Ala Glu Asn Glu Lys Leu Cys Ser Phe
355 360 365

Val Asp Lys Leu Thr Ala Gln Asn Arg Gln Leu Glu Asp Glu Leu Gln
370 375 380

Asp Leu Ala Ala Lys Lys Glu Ser Val Ala His Trp Glu Ala Gln Ile
385 390 395 400

Ala Glu Ile Ile Gln Trp Val Ser Asp Glu Lys Asp Ala Arg Gly Tyr
405 410 415

Leu Gln Ala Leu Ala Ser Lys Met Thr Glu Glu Leu Glu Ala Leu Arg
420 425 430

Ser Ser Ser Leu Gly Ser Arg Thr Leu Asp Pro Leu Trp Lys Val Arg
435 440 445

Arg Ser Gln Lys Leu Asp Met Ser Ala Arg Leu Glu Leu Gln Ser Ala
450 455 460

Leu Glu Ala Glu Ile Arg Ala Lys Gln Leu Val Gln Glu Glu Leu Arg
465 470 475 480

Lys Val Lys Asp Ala Asn Leu Thr Leu Glu Ser Lys Xaa Xaa Asp Ser
485 490 495

Glu Ala Lys Asn Arg Glu Leu Leu Glu Glu Met Glu Ile Leu Lys Lys
500 505 510

Lys Met Glu Glu Lys Phe Arg Ala Asp Thr Gly Leu Lys Leu Pro Asp
515 520 525

Phe Gln Asp Ser Ile Phe Glu Tyr Phe Asn Thr Ala Pro Leu Ala His
530 535 540

Asp Leu Thr Phe Arg Thr Ser Ser Ala Ser Glu Gln Glu Thr Gln Ala
545 550 555 560

Pro Lys Pro Glu Ala Ser Pro Ser Met Ser Val Ala Ala Ser Glu Gln
565 570 575

Gln Glu Asp Met Ala Arg Pro Pro Gln Arg Pro Ser Ala Val Pro Leu
580 585 590

Pro Thr Thr Gln Ala Leu Ala Leu Ala Gly Pro Lys Pro Lys Ala His
595 600 605

Gln Phe Ser Ile Lys Ser Phe Ser Ser Pro Thr Gln Cys Ser His Cys
610 615 620

Thr Ser Leu Met Val Gly Leu Ile Arg Gln Gly Tyr Ala Cys Glu Val
625 630 635 640

Cys Ser Phe Ala Cys His Val Ser Cys Lys Asp Gly Ala Pro Gln Val
645 650 655

Cys Pro Ile Pro Pro Glu Gln Ser Lys Arg Pro Leu Gly Val Asp Val
660 665 670

Gln Arg Gly Ile Gly Thr Ala Tyr Lys Gly His Val Lys Val Pro Lys
675 680 685

Pro Thr Gly Val Lys Lys Gly Trp Gln Arg Ala Tyr Ala Val Val Cys
690 695 700

Asp Cys Lys Leu Phe Leu Tyr Asp Leu Pro Glu Gly Lys Ser Thr Gln
705 710 715 720

Pro Gly Val Ile Ala Ser Gln Val Leu Asp Leu Arg Asp Asp Glu Phe
725 730 735

Ser Val Ser Ser Val Leu Ala Ser Asp Val Ile His Ala Thr Arg Arg
740 745 750

Asp Ile Pro Cys Ile Phe Arg Val Thr Ala Ser Leu Leu Gly Ala Pro
755 760 765

Ser Lys Thr Ser Ser Leu Leu Ile Leu Thr Glu Asn Glu Asn Glu Lys
770 775 780

Arg Lys Trp Val Gly Ile Leu Glu Gly Leu Gln Ser Ile Leu His Lys
785 790 795 800

Asn Arg Leu Arg Asn Gln Val Val His Val Pro Leu Glu Ala Tyr Asp
805 810 815

Ser Ser Leu Pro Leu Ile Lys Ala Ile Leu Thr Ala Ala Ile Val Asp
820 825 830

Ala Asp Arg Ile Ala Val Gly Leu Glu Glu Gly Leu Tyr Val Ile Glu
835 840 845

Val Thr Arg Asp Val Ile Val Arg Ala Ala Asp Cys Lys Lys Val His
850 855 860

Gln Ile Glu Leu Ala Pro Arg Glu Lys Ile Val Ile Leu Leu Cys Gly
865 870 875 880

Arg Asn His His Val His Leu Tyr Pro Trp Ser Ser Leu Asp Gly Ala
885 890 895

Glu Gly Ser Phe Asp Ile Lys Leu Pro Glu Thr Lys Gly Cys Gln Leu
900 905 910

Met Ala Thr Ala Thr Leu Lys Arg Xaa Ser Gly Thr Cys Leu Phe Val
915 920 925

Ala Val Lys Arg Leu Ile Leu Cys Tyr Glu Ile Gln Lys Ile Lys Pro
930 935 940

Tyr
945

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

| | |
|--|------|
| GAGGGCACTT AATCCCAATG AACTGTATGC TTAAAAATAA TTTAAATGAT AAACTTTGTG | 60 |
| TTATGTATAC TTTACCACAA TAAGAAAAAG TATTTTAGTA CTAGTGGTAA ATAGTTTTTA | 120 |
| TTTAATAGAC TTATATTTTA AAGCTTAAAA ATAATTTAGC TTCTAGAGTA TTACGTTTTT | 180 |
| CTTCATGGGA ACTTCAAAAA GCAAGTCACT AAATCCAAGA ATTTTAAAGA AAAAACCCAA | 240 |
| ATACATGATT TATGCTGCAT CTGGTATAGA TTTTAAAAAG ACTAGTCAAT CTAAGCTCTA | 300 |
| AACTATTAAA TGACAAACCA TTCATATGT CATTGCATAT TCCTATGTAC CACATTCTCA | 360 |
| TATTTCTGTT ATGGGCATGA AGGGGTGTTT GATGCTTCCA TGCCATAATA ACCATGACTA | 420 |
| TCACAACCAT TGAAATAAAG GTTCTTGCGT TATTTTCAGG ATGGTCCCAG AAATTTAAAT | 480 |
| TAATCTCTCA TCCATTGGCT TTTGCTACTT TAGGTTAATA TTAAAATATA ACATACATTT | 540 |
| TTGGGGTTTA TGCTGTTAGC TCCAAACCAA AAGATTTTGG AAATTTATTT TGGAAATTTT | 600 |
| GTGTTTAGAA TATGAATAAA TCTGCTTATT CAGAAAAATT AAACCTTGAT AACTTGGGAC | 660 |
| CTCCTATTCC TGTATGTTCT CTGACATACA TTGAGGGATT TGGCTCTCTT TTGTTTATTT | 720 |
| GTTTACTAG TCAGACATTC CTTTGGCTGC CCATACTTAA TTCTGTTGGG TGTTTCCGCC | 780 |
| CCCGCCCTCA GCTTCTGCAG CTACTCTGAT CAACATCCGC AATGCCAGGA AACACTTTGA | 840 |
| AAAGCTGGAA AGAGTGGATG GACCAAAGCA GTGTCTTCTC ATGCGCTAAA CATTGATGAA | 900 |
| TATTGTTTCA CACAAAAATT AAAAGTTTCC TAATTAATGT TGTATTCATA TATGTAGGCT | 960 |
| CTGAAATGTT GTGATGCTTA TTGCTTCTGT ATTTCTTCTC TACTCCCTAG TCTTAATGTT | 1020 |
| TAACCTTGAA TGCTATTAAC TTAAATAGCC ATTGAGGAGT TAGAAGATGA ATTGTTTCATG | 1080 |
| AAGTCGGTGT TACATAAAAG TAGGTGATAT GTAAGTTTTC TGATAACAAG GTTCTAATAG | 1140 |
| TGTTTAAATG TACTGGTAAC CTGGTTCCAA TAGTTGTGTT TGCCCAAGCC TTTCTCGGCA | 1200 |
| TCATCTTGTA TTCCTTATCA GATAGTAAGT AACCTGTAAG TTTGGAGTAT TACTGTTTTC | 1260 |
| TCAGCATGCA TTAAAAATAT TCCTTAACTT CAATTGTAAA AAAAAAAAAA AAAAA | 1315 |

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

```

Met Asn Lys Ser Ala Tyr Ser Glu Lys Leu Asn Leu Asp Asn Leu Gly
1           5           10           15

Pro Pro Ile Pro Val Cys Ser Leu Thr Tyr Ile Glu Gly Phe Gly Ser
          20           25           30

Leu Leu Phe Ile Cys Phe Thr Ser Gln Thr Phe Leu Trp Leu Pro Ile
          35           40           45

Leu Asn Ser Val Gly Cys Phe Arg Pro Arg Pro Gln Leu Leu Gln Leu
          50           55           60

Leu
65

```

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

```

TAGGCCATGA AGGCCGAATC GGCCTTCATG GCCTACGCTT ACACAATACC CACCATGTCC      60
CAGGCTGGTG CTCAGGAAGC CCCTATCAAG AAGAAGCGCC CCCCTGTGAA GGAGGAGGAC      120
CTGAAGGGGG CCCGAGGAAA CCTGACCAAG AACCAGGAAA TCAAGTCCAA GACCTACCAG      180
GTCATGCGAG AGTGTGAGCA AGCTGGCTCG GCCGCCCCGT CGGTGTTTCAG CCGCACCCGC      240
ACAGGTACCG AGACTGTCTT TGAGAAGCCC AAAGCCGGAC CCACCAAGAG TGTCTTCGGC      300
TGAGAAGTGT GCGCCACTCC CCTTGCTGCC CGAATGCTCG GAAACAGGAG CCTTACCCAG      360
GAACTCTTTT TTATGCCAGA ACGCTTCCTC TCCCCTGCTG TCTCTGGGGC TGCCACCCTC      420

```

CCCCACAGTC CAGGCCCTTC AGCCAAGGGC TCTGCACCAG CACCTTGGAA GCACCAATAA 480
AGAGGATGCC CACGTGGCCC CAGCAAAAAA AAAAAAAAAA 519

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Lys | Ala | Glu | Ser | Ala | Phe | Met | Ala | Tyr | Ala | Tyr | Thr | Ile | Pro | Thr | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Met | Ser | Gln | Ala | Gly | Ala | Gln | Glu | Ala | Pro | Ile | Lys | Lys | Lys | Arg | Pro | |
| | | | 20 | | | | | 25 | | | | | | 30 | | |
| Pro | Val | Lys | Glu | Glu | Asp | Leu | Lys | Gly | Ala | Arg | Gly | Asn | Leu | Thr | Lys | |
| | | | 35 | | | | 40 | | | | | 45 | | | | |
| Asn | Gln | Glu | Ile | Lys | Ser | Lys | Thr | Tyr | Gln | Val | Met | Arg | Glu | Cys | Glu | |
| | | | 50 | | | 55 | | | | | 60 | | | | | |
| Gln | Ala | Gly | Ser | Ala | Ala | Pro | Ser | Val | Phe | Ser | Arg | Thr | Arg | Thr | Gly | |
| | | | 65 | | | 70 | | | | 75 | | | | | 80 | |
| Thr | Glu | Thr | Val | Phe | Glu | Lys | Pro | Lys | Ala | Gly | Pro | Thr | Lys | Ser | Val | |
| | | | 85 | | | | | | 90 | | | | | 95 | | |
| Phe | Gly | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2788 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| GACGGCGACC | AAACCCAGCT | AGGTCAGACG | AGAAAGATAA | AAACTCTCCA | GATGTCTTCC | 60 |
| AGTAATGTCTG | AAGTTTTTAT | CCCAGTGTCA | CAAGGAAACA | CCAATGGCTT | CCCCGCGACA | 120 |
| GCTTCCAATG | ACCTGAAGGC | ATTTACTGAA | GGAGCTGTGT | TAAGTTTTC | TAACATCTGC | 180 |

| | | | | | | |
|------------|------------|------------|-------------|-------------|-------------|------|
| TATCGAGTAA | AACTGAAGAG | TGGCTTTCTA | CCTTGTCGAA | AACCAGTTGA | GAAAGAAATA | 240 |
| TTATCGAATA | TCAATGGGAT | CATGAAACCT | GGTCTCAACG | CCATCCTGGG | ACCCACAGGT | 300 |
| GGARGCAAAT | CTTCGTTATT | AGATGTCTTA | GCTGCAAGGA | AAGATCCAAG | TGGATTATCT | 360 |
| GGAGATGTTT | TGATAAATGG | AGCACCGCGA | CCTGCCAATT | TCAAATGTAA | TTCAGGTTAC | 420 |
| GTGGTACAAG | TTGGAACCTA | GTTTATCCGT | GGTGTGTCTG | GAGGAGAAAG | AAAAAGGACT | 480 |
| AGTATAGGAA | TGGAGCTTAT | CACTGATCCT | TCCATCTTGT | TCTTGATGA | GCCTACAACCT | 540 |
| GGCTTAGACT | CAAGCACAGC | AAATGCTGTC | CTTTTGCTCC | TGAAAAGGAT | GTCTAAGCAG | 600 |
| GGACGAACAA | TCATCTTCTC | CATTCATCAG | CCTCGATATT | CCATCTTCAA | GTTGTTTGAT | 660 |
| AGCCTCACCT | TATTGGCCTC | AGGAAGACTT | ATGTTCCACG | GGCCTGCTCA | GGAGGCCTTG | 720 |
| GGATACTTTG | AATCAGCTGG | TTATCACTGT | GAGGCCTATA | ATAACCCTGC | AGACTTCTTC | 780 |
| TTGGACATCA | TTAATGGAGA | TTCCACTGCT | GTGGCATTAA | ACAGAGAAGA | AGACTTTAAA | 840 |
| GCCACAGAGA | TCATAGAGCC | TTCCAAGCAG | GATAAGCCAC | TCATAGAAAA | ATTAGCGGAG | 900 |
| ATTTATGTCA | ACTCCTCCTT | CTACAAAGAG | ACAAAAGCTG | AATTACATCA | ACTTTCCGGG | 960 |
| GGTGAGAAGA | AGAAGAAGAT | CACAGTCTTC | AAGGAGATCA | GCTACACCAC | CTCCTTCTGT | 1020 |
| CATCAACTCA | GATGGGTTTC | CAAGCGTTCA | TTCAAAAACCT | TGCTGGGTAA | TCCCCAGGCC | 1080 |
| TCTATAGCTC | AGATCATTGT | CACAGTCGTA | CTGGGACTGG | TTATAGGTGC | CATTTACTTT | 1140 |
| GGGCTAAAAA | ATGATTCTAC | TGGAATCCAG | AACAGAGCTG | GGGTCTCTCT | CTTCCTGACG | 1200 |
| ACCAACCAGT | GTTTCAGCAG | TGTTTCAGCC | GTGGAACCTC | TTGTGGTAGA | GAAGAAGCTC | 1260 |
| TTCATACATG | AATACATCAG | CGGATACTAC | AGAGTGTCAT | CTTATTTCCCT | TGGAAAACCTG | 1320 |
| TTATCTGATT | TATTACCCAT | GAGGATGTTA | CCAAGTATTA | TATTTACCTG | TATAGTGATC | 1380 |
| TTCATGTTAG | GATTGAAGCC | AAAGGCAGAT | GCCTTCTTCG | TTATGATGTT | TACCCTTATG | 1440 |
| ATGGTGGCTT | ATTCAGCCAG | TTCCATGGCA | CTGGCCATAG | CAGCAGGTCA | GAGTGTGGTT | 1500 |
| TCTGTAGCAA | CACTTCTCAT | GACCATCTGT | TTGTGTGTTA | TGATGATTTT | TTCAGGTCTG | 1560 |
| TTGGTCAATC | TCACAACCAT | TGCATCTTGG | CTGTCATGGC | TTCAGTACTT | CAGCATTCCA | 1620 |
| CGATATGGAT | TTACGGCTTT | GCAGCATAAT | GAATTTTGG | GACAAAACCT | CTGCCAGGA | 1680 |
| CTCAATGCAA | CAGGAAACAA | TCCTTGTAAC | TATGCAACAT | GTAAGGCGA | AGAATATTTG | 1740 |
| GTAAAGCAGG | GCATCGATCT | CTCACCTTGG | GGCTTGTGGA | AGAATCACGT | GGCCTTGGCT | 1800 |
| TGTATGATTG | TTATTTTCCT | CACAATTGCC | TACCTGAAAT | TGTTATTTCT | TAAAAAATAT | 1860 |

TCTTAAATTT CCCCTTAATT CAGTATGATT TATCCTCACA TAAAAAGAA GCACTTTGAT 1920
TGAAGTATTC AATCAAGTTT TTTTGGTTGT TTTCTGTTCC CTTGCCATCA CACTGTTGCA 1980
CAGCAGCAAT TGTTTTAAAG AGATACATTT TTAGAAATCA CAACAACTG AATTAAACAT 2040
GAAAGAACCC AAGACATCAT GTATCGCATA TTAGTTAATC TCCTCAGACA GTAACCATGG 2100
GGAAGAAATC TGGTCTAATT TATTAATCTA AAAAAGGAGA ATTGAATTCT GGAAACTCCT 2160
GACAAGTTAT TACTGTCTCT GGCATTTGTT TCCTCATCTT TAAAATGAAT AGGTAGGTTA 2220
GTAGCCCTTC AGTCTTAATA CTTTATGATG CTATGGTTTG CCATTATTTA ATAAATGACA 2280
AATGTATTAA TGCTAAAAAA AAAAAAAAAA AGCGGCCTTC ATGGCCTAGA GATTTCAACT 2340
TAACTTGACC GCTCTGAGCT AAACCTAGCC CCAAACCCAC TCCACCTTAT TACCAGACAA 2400
CCTTAACCAA ACCATTTACC CAAATAAAGT ATAGGCGATA GAAATTGAAA CCTGGCGCAA 2460
TAGATATAGT ACCGCAAGGG AAAGATGAAA AATTATAACC AAGCATAATA TAGCAAGGAC 2520
TAACCCCTAT ACCTTCTGCA TAATGAATTA ACTAGAAATA ACTTTGCAAG GAGAGCCAAA 2580
GCTAAGACCC CCGAAACCAG ACGAGCTACC TAAGAACAGC TAAAAGAGCA CACCCGTCTA 2640
TGTAGCAAAA TAGTGGGAAG ATTTATAGGT AGAGGCGACA AACCTACCGA GCCTGGTGAT 2700
AGCTGGTTGT CCCAGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2760
AAAAAAAAA AAAAAAAAAA AAAAAAAA 2788

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Met Ser Ser Ser Asn Val Glu Val Phe Ile Pro Val Ser Gln Gly Asn
1 5 10 15
Thr Asn Gly Phe Pro Ala Thr Ala Ser Asn Asp Leu Lys Ala Phe Thr
20 25 30
Glu Gly Ala Val Leu Ser Phe His Asn Ile Cys Tyr Arg Val Lys Leu
35 40 45
Lys Ser Gly Phe Leu Pro Cys Arg Lys Pro Val Glu Lys Glu Ile Leu
50 55 60

Ser Asn Ile Asn Gly Ile Met Lys Pro Gly Leu Asn Ala Ile Leu Gly
65 70 75 80

Pro Thr Gly Gly Xaa Lys Ser Ser Leu Leu Asp Val Leu Ala Ala Arg
85 90 95

Lys Asp Pro Ser Gly Leu Ser Gly Asp Val Leu Ile Asn Gly Ala Pro
100 105 110

Arg Pro Ala Asn Phe Lys Cys Asn Ser Gly Tyr Val Val Gln Val Gly
115 120 125

Thr Gln Phe Ile Arg Gly Val Ser Gly Gly Glu Arg Lys Arg Thr Ser
130 135 140

Ile Gly Met Glu Leu Ile Thr Asp Pro Ser Ile Leu Phe Leu Asp Glu
145 150 155 160

Pro Thr Thr Gly Leu Asp Ser Ser Thr Ala Asn Ala Val Leu Leu Leu
165 170 175

Leu Lys Arg Met Ser Lys Gln Gly Arg Thr Ile Ile Phe Ser Ile His
180 185 190

Gln Pro Arg Tyr Ser Ile Phe Lys Leu Phe Asp Ser Leu Thr Leu Leu
195 200 205

Ala Ser Gly Arg Leu Met Phe His Gly Pro Ala Gln Glu Ala Leu Gly
210 215 220

Tyr Phe Glu Ser Ala Gly Tyr His Cys Glu Ala Tyr Asn Asn Pro Ala
225 230 235 240

Asp Phe Phe Leu Asp Ile Ile Asn Gly Asp Ser Thr Ala Val Ala Leu
245 250 255

Asn Arg Glu Glu Asp Phe Lys Ala Thr Glu Ile Ile Glu Pro Ser Lys
260 265 270

Gln Asp Lys Pro Leu Ile Glu Lys Leu Ala Glu Ile Tyr Val Asn Ser
275 280 285

Ser Phe Tyr Lys Glu Thr Lys Ala Glu Leu His Gln Leu Ser Gly Gly
290 295 300

Glu Lys Lys Lys Lys Ile Thr Val Phe Lys Glu Ile Ser Tyr Thr Thr
305 310 315 320

Ser Phe Cys His Gln Leu Arg Trp Val Ser Lys Arg Ser Phe Lys Asn
325 330 335

Leu Leu Gly Asn Pro Gln Ala Ser Ile Ala Gln Ile Ile Val Thr Val
340 345 350

Val Leu Gly Leu Val Ile Gly Ala Ile Tyr Phe Gly Leu Lys Asn Asp
355 360 365

Ser Thr Gly Ile Gln Asn Arg Ala Gly Val Leu Phe Phe Leu Thr Thr
370 375 380

Asn Gln Cys Phe Ser Ser Val Ser Ala Val Glu Leu Phe Val Val Glu
385 390 395 400

Lys Lys Leu Phe Ile His Glu Tyr Ile Ser Gly Tyr Tyr Arg Val Ser
405 410 415

Ser Tyr Phe Leu Gly Lys Leu Leu Ser Asp Leu Leu Pro Met Arg Met
420 425 430

Leu Pro Ser Ile Ile Phe Thr Cys Ile Val Tyr Phe Met Leu Gly Leu
435 440 445

Lys Pro Lys Ala Asp Ala Phe Phe Val Met Met Phe Thr Leu Met Met
450 455 460

Val Ala Tyr Ser Ala Ser Ser Met Ala Leu Ala Ile Ala Ala Gly Gln
465 470 475 480

Ser Val Val Ser Val Ala Thr Leu Leu Met Thr Ile Cys Phe Val Phe
485 490 495

Met Met Ile Phe Ser Gly Leu Leu Val Asn Leu Thr Thr Ile Ala Ser
500 505 510

Trp Leu Ser Trp Leu Gln Tyr Phe Ser Ile Pro Arg Tyr Gly Phe Thr
515 520 525

Ala Leu Gln His Asn Glu Phe Leu Gly Gln Asn Phe Cys Pro Gly Leu
530 535 540

Asn Ala Thr Gly Asn Asn Pro Cys Asn Tyr Ala Thr Cys Thr Gly Glu
545 550 555 560

Glu Tyr Leu Val Lys Gln Gly Ile Asp Leu Ser Pro Trp Gly Leu Trp
565 570 575

Lys Asn His Val Ala Leu Ala Cys Met Ile Val Ile Phe Leu Thr Ile
580 585 590

Ala Tyr Leu Lys Leu Leu Phe Leu Lys Lys Tyr Ser
595 600

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2930 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| CGACTTCCTC | GGCTGCGCGG | CGCTCGCGCG | GAGCTCCCCG | GCCGGCGGTG | CGTCCCCACG | 60 |
| GTCACCATGA | AAGACGACTT | CGCAGAGGAG | GAGGAGGTGC | AATCCTTCGG | TTACAAGCGG | 120 |
| TTTGGTATTC | AGGAAGGAAC | ACAATGTACC | AAATGTAAAA | ATAACTGGGC | ACTGAAGTTT | 180 |
| TCTATCATAT | TATTATACAT | TTTGTGTGCC | TTGCTAACAA | TCACAGTAGC | CATTTTGGGA | 240 |
| TATAAAGTTG | TAGAGAAAAT | GGACAATGTC | ACAGGTGGCA | TGAAACATC | TCGCCAAACC | 300 |
| TATGATGACA | AGCTCACAGC | AGTGAAAGT | GACCTGAAAA | AATTAGGTGA | CCAAACTGGG | 360 |
| AAGAAAGCTA | TCAGCACCAA | CTCAGAACTC | TCCACCTTCA | GATCAGACAT | TCTAGATCTC | 420 |
| CGTCAGCAAC | TTCGTGAGAT | TACAGAAAAA | ACCAGCAAGA | ACAAGGATAC | GCTGGAGAAG | 480 |
| TTACAGGCGA | GCGGGGATGC | TCTGGTGGAC | AGGCAGAGTC | AATTGAAAGA | AACTTTGGAG | 540 |
| AATAACTCTT | TCCTCATCAC | CACTGTAAAC | AAAACCCTCC | AGGCGTATAA | TGGCTATGTC | 600 |
| ACGAATCTGC | AGCAAGATAC | CAGCGTGCTC | CAGGGCAATC | TGCAGAACCA | AATGTATTCT | 660 |
| CATAATGTGG | TCATCATGAA | CTCAACAACC | TGAACCTGAC | CCAGGTGCAG | CAGAGGAACC | 720 |
| TCATCACGAA | TCTGCAGCGG | TCTGTGGATG | ACACAAGCCA | GGCTATCCAG | CGAATCAAGA | 780 |
| ACGACTTTCA | AAATCTGCAG | CAGGTTTTTC | TTCAAGCCAA | GAAGGACACG | GATTGGCTGA | 840 |
| AGGAGAAAGT | GCAGAGCTTG | CAGACGCTGG | CTGCCAACAA | CTCTGCGTTG | GCCAAAGCCA | 900 |
| ACAACGACAC | CCTGGAGGAT | ATGAACAGCC | AGCTCAACTC | ATTCACAGGT | CAGATGGAGA | 960 |
| ACATCACCAC | TATCTCTCAA | GCCAACGAGC | AGAACCTGAA | AGACCTGCAG | GACTTACACA | 1020 |
| AAGATGCAGA | GAATAGAACA | GCCATCAAGT | TCAACCAACT | GGAGGAACGC | TTCCAGCTCT | 1080 |
| TTGAGACGGA | TATTGTGAAC | ATCATTAGCA | ATATCAGTTA | CACAGCCCAC | CACCTGCGGA | 1140 |
| CGCTGACCAG | CAATCTAAAT | GAAGTCAGGA | CCACTTGCAC | AGATACCCTT | ACCAAACACA | 1200 |
| CAGATGATCT | GACCTCCTTG | AATAATACCC | TGGCCAACAT | CCGTTTGGAT | TCTGTTTCTC | 1260 |
| TCAGGATGCA | ACAAGATTTG | ATGAGGTCGA | GGTTAGACAC | TGAAGTAGCC | AACTTATCAG | 1320 |
| TGATTATGGA | AGAAATGAAG | CTAGTAGACT | CCAAGCATGG | TCAGCTCATC | AAGAATTTTA | 1380 |
| CAATACTACA | AGGTCCACCG | GGCCCCAGGG | GTCCAAGAGG | TGACAGAGGA | TCCCAGGGAC | 1440 |
| CCCCTGGCCC | AACTGGCAAC | AAGGGACAGA | AAGGAGAGAA | GGGGGAGCCT | GGACCACCTG | 1500 |
| GCCCTGCGGG | TGAGAGAGGC | CCAATTGGAC | CAGCTGGTCC | CCCCGAGAG | CGTGGCGGCA | 1560 |
| AAGGATCTAA | AGGCTCCCAG | GGCCCCAAAG | GCTCCCGTGG | TTCCCCTGGG | AAGCCCGGCC | 1620 |
| CTCAGGGCCC | CAGTGGGGAC | CCAGGCCCCC | CGGGCCCACC | AGGCAAAGAG | GGACTCCCCG | 1680 |

| | |
|---|------|
| GCCCTCAGGG CCCTCCTGGC TTCCAGGGAC TTCAGGGCAC CGTTGGGGAG CCTGGGGTGC | 1740 |
| CTGGACCTCG GGGACTGCCA GGCTTGCCTG GGGTACCAGG CATGCCAGGC CCCAAGGGCC | 1800 |
| CCCCGGCCCC TCCTGGCCCA TCAGGAGCGG TGGTGCCCTT GGCCCTGCAG AATGAGCCAA | 1860 |
| CCCCGGCACC GGAGGACAAT AGCTGCCCCG CACTACTGGAA GAACTTCACA GACAAATGCT | 1920 |
| ACTATTTTTC AGTTGAGAAA GAAATTTTGT AGGATGCAAA GCTTTTCTGT GAAGACAAGT | 1980 |
| CTTCACATCT TGTTTTTATA AACACTAGAG AGGAACAGCA ATGGATAAAA AAACAGATGG | 2040 |
| TAGGGAGAGA GAGCCACTGG ATCGGCCTCA CAGACTCAGA GCGTGAAAAAT GAATGGAAAGT | 2100 |
| GGCTGGATGG GACATCTCCA GACTACAAAA ATTGGAAAGC TGGACAGCCG GATAACTGGG | 2160 |
| GTCATGGCCA TGGGCCAGGA GAAGACTGTG CTGGGTTGAT TTATGCTGGG CAGTGAACG | 2220 |
| ATTTCCAATG TGAAGACGTC AATAACTTCA TTTGCGAAAA AGACAGGGAG ACAGTACTGT | 2280 |
| CATCTGCATT ATAACGGACT GTGATGGGAT CACATGAGCA AATTTTCAGC TCTCAAAGGC | 2340 |
| AAAGGACACT CCTTTCTAAT TGCATCACCT TCTCATCAGA TTGAAAAAAAA AAAAGCACTG | 2400 |
| AAAGCCAATT ACTGAAAAAAAA AATTGACAGC TAGTGTTTTT TACCATCCGT CATTACCCAA | 2460 |
| AGACTTGGGA ACTAAAAATGT TCCCCAGGGT GATATGCTGA TTTTCATTGT GCACATGGAC | 2520 |
| TGAATCACAT AGATTCTCCT CCGTCAGTAA CCGTGCGATT ATACAAATTA TGTCTTCCAA | 2580 |
| AGTATGGAAC ACTCCAATCA GAAAAAGGTT ATCATTGGTC GTTGAGTTAT GGGAAGAACT | 2640 |
| TAAGCATATA CTGTGTAAAC AGTGCCATAC ATTTCTAAAA TCCAAGTGT AGGAAAAATA | 2700 |
| TGCAGACATA CAGATATATA GGCCAACTAT TAGTAATAAT ATGAAATATA CTAAAGAGC | 2760 |
| TTTTAAAACT TTGTATTTTT GTACAAAATA TTTGTCTTTT ACAATTTTTT TCCTTTTTTT | 2820 |
| TTTTTTGTCA TTTTACCGAC ATAATACATG GAGCCAAAGA AAACAATAAT GGTACTAATA | 2880 |
| AAAACCTCCTA GGGTTTCCTG TCAGATTTAA TTCTAAAAA AAAAAAAAAA | 2930 |

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Met Lys Asp Asp Phe Ala Glu Glu Glu Glu Val Gln Ser Phe Gly Tyr

| | | | |
|---|-----|-----|-----|
| 1 | 5 | 10 | 15 |
| Lys Arg Phe Gly Ile Gln Glu Gly Thr Gln Cys Thr Lys Cys Lys Asn | | | |
| 20 | 25 | 30 | |
| Asn Trp Ala Leu Lys Phe Ser Ile Ile Leu Leu Tyr Ile Leu Cys Ala | | | |
| 35 | 40 | 45 | |
| Leu Leu Thr Ile Thr Val Ala Ile Leu Gly Tyr Lys Val Val Glu Lys | | | |
| 50 | 55 | 60 | |
| Met Asp Asn Val Thr Gly Gly Met Glu Thr Ser Arg Gln Thr Tyr Asp | | | |
| 65 | 70 | 75 | 80 |
| Asp Lys Leu Thr Ala Val Glu Ser Asp Leu Lys Lys Leu Gly Asp Gln | | | |
| 85 | 90 | 95 | |
| Thr Gly Lys Lys Ala Ile Ser Thr Asn Ser Glu Leu Ser Thr Phe Arg | | | |
| 100 | 105 | 110 | |
| Ser Asp Ile Leu Asp Leu Arg Gln Gln Leu Arg Glu Ile Thr Glu Lys | | | |
| 115 | 120 | 125 | |
| Thr Ser Lys Asn Lys Asp Thr Leu Glu Lys Leu Gln Ala Ser Gly Asp | | | |
| 130 | 135 | 140 | |
| Ala Leu Val Asp Arg Gln Ser Gln Leu Lys Glu Thr Leu Glu Asn Asn | | | |
| 145 | 150 | 155 | 160 |
| Ser Phe Leu Ile Thr Thr Val Asn Lys Thr Leu Gln Ala Tyr Asn Gly | | | |
| 165 | 170 | 175 | |
| Tyr Val Thr Asn Leu Gln Gln Asp Thr Ser Val Leu Gln Gly Asn Leu | | | |
| 180 | 185 | 190 | |
| Gln Asn Gln Met Tyr Ser His Asn Val Val Ile Met Asn Ser Thr Thr | | | |
| 195 | 200 | 205 | |

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1589 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

| | |
|---|-----|
| TCTATATATT TTTTCTAGGA AGGGGTGTTT TTCTTTCTGA TTTAATTCCC TACATTTTTC | 60 |
| TCTTTCATAT GAAGTTGCAG ATAATGTTTT TCCTTCGGAT TTTTATTCTT TAAGATTTTT | 120 |
| AACCTGTGCA AGACTTTTTC AATGATACAA GTCAAGGAGG ATGAAGATCT TTTTCCACTT | 180 |

CAGTCTTCAC TTTGCTCCAG CTATTGCTAA GAAAGGCACA AACAATGACA GCATATTTAA 240
 GGAAGAACCT GGCCGGCTTG GGTACCGCT GCTGTCTTTC TTGGTTTTGC GTCTACCTGG 300
 GAGAGCCCAG CTTTATAGGT CCCATTGAGG GAAGCATGAG AGAGGATTGT TTGGGGGATG 360
 CTGCCAGAGC TTCCAGCTGA CAGTCTCTGC AGAGCGGCTG CCAAGTGGCC TGGTGGCCGT 420
 ATGTTGGCAG TTTTGTATGA ATTGGGATTA GGAATGTTT GTTTACTTGA TAACCGAGTG 480
 TCTACAAGGA GAGGTGGCAG CGTGAGGGAA TAGTGCCACC ATAATGAGGA CACAGCCAGC 540
 CATCTCTTCC CTGCCACAGA ACCCCAGGCA GTCCCCTTCA GGCTACAGTT TTCCATCTGG 600
 ACCGAGGGAC TGGCCGGTGC AGCAGGAGGA GCCGATCACC CTCTGTGGGA ACGAGGATGC 660
 CCAGAAGTTC CAGTTACTGT GGCTCCATGG TCCCCTTCTC GATGCGCATC TTGCACGCGG 720
 AGCTTCAGCA GTACCTGGGG AACCACAGG AGTCGCTGGA TAGACTGCAC AAGGTGAAGA 780
 CTGTCTGCAG CAAGATCCTG GCCAATTTGG AGCAAGGCTT AGCAGAAGAC GGCGGCATGA 840
 GCAGCGTGAC TCAGGAGGGC AGACAAGCCT CTATCCGGCT GTGGAGGTCA CGTCTGGGCC 900
 GGGTGATGTA CTCCATGGCA AACTGTCTGC TCCTGATGAA GGATTATGTG CTGGCCGTGG 960
 AGGCGTATCA TTCGGTTATC AAGTATTACC CAGAGCAAGA GCCCCAGCTG CTCAGCGGCA 1020
 TCGGCCGGAT TTCCCTGCAG ATTGGAGACA TAAAAACAGC TGAAAAGTAT TTTCAAGACG 1080
 TTGAGAAAGT AACACAGAAA TTAGATGGAC TACAGGGTAA AATCATGGTT TTGATGAACA 1140
 GCGCGTTCCT TCACCTCGGG CAGAATAACT TTGCAGAAAGC CCACAGGTTC TTCACAGAGA 1200
 TCTTAAGGAT GGATCCAAGA AACGCAGTGG CCAACAACAA CGCTGCCGTG TGTCTGCTCT 1260
 ACCTGGGCAA GCTCAAGGAC TCCCTGCGGC AGCTGGAGGC CATGGTCCAG CAGGACCCCA 1320
 GGCACCTACCT GCACGAGAGC GTGCTCTTCA ACCTGACCAC CATGTACGAG CTGGAGTCCT 1380
 CACGGAGCAT GCAGAAGAAA CAGGCCCTGC TGGAGGCTGT CGCCGGCAAG GAGGGGGACA 1440
 GCTTCAACAC ACAGTGCCTC AAGCTGGCCT AGCTGCCTCC AACACACTAC GTCAGAAGGA 1500
 CCCGGGTCTT TGAAACTGTG TCTTGAAGCT AATGTATTAA TGTGACATGG AGGAACTCAA 1560
 TAAAACTCCT GCTTCAAAAA AAAAAAAAAA 1589

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Arg | Ser | Ser | Ser | Tyr | Cys | Gly | Ser | Met | Val | Pro | Phe | Ser | Met | 1 | 5 | 10 | 15 |
| Arg | Ile | Leu | His | Ala | Glu | Leu | Gln | Gln | Tyr | Leu | Gly | Asn | Pro | Gln | Glu | 20 | 25 | 30 | |
| Ser | Leu | Asp | Arg | Leu | His | Lys | Val | Lys | Thr | Val | Cys | Ser | Lys | Ile | Leu | 35 | 40 | 45 | |
| Ala | Asn | Leu | Glu | Gln | Gly | Leu | Ala | Glu | Asp | Gly | Gly | Met | Ser | Ser | Val | 50 | 55 | 60 | |
| Thr | Gln | Glu | Gly | Arg | Gln | Ala | Ser | Ile | Arg | Leu | Trp | Arg | Ser | Arg | Leu | 65 | 70 | 75 | 80 |
| Gly | Arg | Val | Met | Tyr | Ser | Met | Ala | Asn | Cys | Leu | Leu | Leu | Met | Lys | Asp | 85 | 90 | 95 | |
| Tyr | Val | Leu | Ala | Val | Glu | Ala | Tyr | His | Ser | Val | Ile | Lys | Tyr | Tyr | Pro | 100 | 105 | 110 | |
| Glu | Gln | Glu | Pro | Gln | Leu | Leu | Ser | Gly | Ile | Gly | Arg | Ile | Ser | Leu | Gln | 115 | 120 | 125 | |
| Ile | Gly | Asp | Ile | Lys | Thr | Ala | Glu | Lys | Tyr | Phe | Gln | Asp | Val | Glu | Lys | 130 | 135 | 140 | |
| Val | Thr | Gln | Lys | Leu | Asp | Gly | Leu | Gln | Gly | Lys | Ile | Met | Val | Leu | Met | 145 | 150 | 155 | 160 |
| Asn | Ser | Ala | Phe | Leu | His | Leu | Gly | Gln | Asn | Asn | Phe | Ala | Glu | Ala | His | 165 | 170 | 175 | |
| Arg | Phe | Phe | Thr | Glu | Ile | Leu | Arg | Met | Asp | Pro | Arg | Asn | Ala | Val | Ala | 180 | 185 | 190 | |
| Asn | Asn | Asn | Ala | Ala | Val | Cys | Leu | Leu | Tyr | Leu | Gly | Lys | Leu | Lys | Asp | 195 | 200 | 205 | |
| Ser | Leu | Arg | Gln | Leu | Glu | Ala | Met | Val | Gln | Gln | Asp | Pro | Arg | His | Tyr | 210 | 215 | 220 | |
| Leu | His | Glu | Ser | Val | Leu | Phe | Asn | Leu | Thr | Thr | Met | Tyr | Glu | Leu | Glu | 225 | 230 | 235 | 240 |
| Ser | Ser | Arg | Ser | Met | Gln | Lys | Lys | Gln | Ala | Leu | Leu | Glu | Ala | Val | Ala | 245 | 250 | 255 | |
| Gly | Lys | Glu | Gly | Asp | Ser | Phe | Asn | Thr | Gln | Cys | Leu | Lys | Leu | Ala | | 260 | 265 | 270 | |

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

| | |
|---|------|
| TATAAAGAGT GACTCTCCTA TGAAGGTAAA GGCCACCCCT CTTCACTTCC AGTGACTGAG | 60 |
| ATACATTTTT CCAATCCTGG GGGCAAATAC AGACACAGCA AGTTCCTTCT TCCCTTTGGA | 120 |
| AATTTGGCAG CTGCCTTCAC CAGTGAGCAC AAAGCCACAT TTCAAAGGAA ACTGACAAAT | 180 |
| TATCCCCAGC TGCCAGAAGA AGAAATCCTC ACTGGACGGC TTCCTGTTTC CTGTGGTTCA | 240 |
| TTATCTGATT GGCTGCAGGG ATGAAAGTTT TTAAGTTCAT AGGACTGATG ATCCTCCTCA | 300 |
| CCTCTGCGTT TTCAGCCGGT TCAGGACAAA GTCCAATGAC TGTGCTGTGC TCCATAGACT | 360 |
| GGTTCATGGT CACAGTGCAC CCCTTCATGC TAAACAACGA TGTGTGTGTA CACTTTCATG | 420 |
| AACTACACTT GGGCCTGGGT TGCCCCCAA ACCATGTTCA GCCACACGCC TACCAGTTCA | 480 |
| CCTACCGTGT TACTGAATGT GGCATCAGGG CCAAAGCTGT CTCTCAGGAC ATGGTTATCT | 540 |
| ACAGCACTGA GATACACTAC TCTTCTAAGG GCACGCCATC TAAGTTTGTG ATCCCAGTGT | 600 |
| CATGTGCTGC CCCCCAAAAG TCCCCATGGC TCACCAAGCC CTGCTCCATG AGAGTAGCCA | 660 |
| GCAAGAGCAG GGCCACAGCC CAGAAGGATG AGAAATGCTA CGAGGTGTTC AGCTTGTCAC | 720 |
| AGTCCAGTCA AAGGCCCAAC TGCGATTGTC CACCTTGTGT CTTCACTGAA GAAGAGCATA | 780 |
| CCCAGGTCCC TTGTCACCAA GCAGGGGCTC AGGAGGCTCA ACCTCTGCAG CCATCTCACT | 840 |
| TTCTTGATAT TTCTGAGGAT TGGTCTCTTC ACACAGATGA TATGATTGGG TCCATGTGAT | 900 |
| CCTCAGGTTT GGGGTCTCCT GAAGATGCTA TTTCTAGAAT TAGTATATAG TGTACAAATG | 960 |
| TCTGACAAAT AAGTGCTCTT GTGACCCTCA TGTGAGCACT TTTGAGAAAG AGAAACCTAT | 1020 |
| AGCAACTTCA TGAATTAAGC CTTTTTCTAT ATTTTATAT TCATGTGTAA ACAAAAAATA | 1080 |
| AAATAAAATT CTGATCGCAT AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA | 1140 |
| AAAAAAAAAA AAA | 1153 |

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

```

Met Lys Val Phe Lys Phe Ile Gly Leu Met Ile Leu Leu Thr Ser Ala
1           5           10           15

Phe Ser Ala Gly Ser Gly Gln Ser Pro Met Thr Val Leu Cys Ser Ile
          20           25           30

Asp Trp Phe Met Val Thr Val His Pro Phe Met Leu Asn Asn Asp Val
          35           40           45

Cys Val His Phe His Glu Leu His Leu Gly Leu Gly Cys Pro Pro Asn
          50           55           60

His Val Gln Pro His Ala Tyr Gln Phe Thr Tyr Arg Val Thr Glu Cys
65           70           75           80

Gly Ile Arg Ala Lys Ala Val Ser Gln Asp Met Val Ile Tyr Ser Thr
          85           90           95

Glu Ile His Tyr Ser Ser Lys Gly Thr Pro Ser Lys Phe Val Ile Pro
          100          105          110

Val Ser Cys Ala Ala Pro Gln Lys Ser Pro Trp Leu Thr Lys Pro Cys
          115          120          125

Ser Met Arg Val Ala Ser Lys Ser Arg Ala Thr Ala Gln Lys Asp Glu
          130          135          140

Lys Cys Tyr Glu Val Phe Ser Leu Ser Gln Ser Ser Gln Arg Pro Asn
145          150          155          160

Cys Asp Cys Pro Pro Cys Val Phe Ser Glu Glu Glu His Thr Gln Val
          165          170          175

Pro Cys His Gln Ala Gly Ala Gln Glu Ala Gln Pro Leu Gln Pro Ser
          180          185          190

His Phe Leu Asp Ile Ser Glu Asp Trp Ser Leu His Thr Asp Asp Met
          195          200          205

Ile Gly Ser Met
          210

```

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4285 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

| | |
|---|------|
| TTTAATCTGT GTCTCCAGCA TTTATTTTTT TGTTTGTGTC ATCGGGTTCC TGGTTTTCTT | 60 |
| TTAAGACATA GTCAACTGTG TGGACCTGTA GGT TTGGGGC AGCAACCAAT TCCATTGTTT | 120 |
| TCCTTTTTGT CAAATCCAAG AGAAAATATA CCATAAGGAG CTAGAAGATT CTAGTTCACA | 180 |
| GCCTTTTGAA TCTTCATGGC CTTTGAATCC TCATGGCCTC TGAAATCTGA ATCAGTTTTT | 240 |
| TCCCAGGARG TCTCTGGGGG CTGAGCTGCT ACAGGGGCGAR ARGGTGGGGT GGGGTGGGT | 300 |
| GGGARAATCA TCCTGGCACT TCATCGTGCA TGCTATTTTCG GGCAGCATCT TTTTTTTTTT | 360 |
| ATTTTATTAT TATTTTTTTTTT CCTGATGCTT GAGTTATGAA TGAGGATGAC CTCTGCAATC | 420 |
| ATGATGTCTC CCATAGACTC TGTTCCCTGT TCCTTTGCCA GCTTTCCTCAT GCATGGTCCT | 480 |
| AACACTTCCA TGATTTAATC TGCTGCAGGA CCATAGTCTT CAGCCACCTC AGCAATAACT | 540 |
| TGTTAGAACA TTAAGAGGAA GTAAATTGAG AACAACTTGT TGCCATCCCA TTTTCATTAG | 600 |
| AAATCAGACA TCTTAGAGAT GTCAAGAAAG CAGCTAGCAG CTAGGGGGTA TGGGGACCTG | 660 |
| TCCTGCTCAC ACTGCTGTGT GTCAGACCAG ACCTGATCCT GGAGCTCAGG ACCCTAGAGA | 720 |
| GCCCTGATCT CTGGAACCTT TGCCACGTTG TTGCTGAGGC AGCTGAAGTC CCCATCTCCC | 780 |
| ACCATAACAA TCACAAATAG ACAGTAGTGG AGCCAGCATC CCCAGGCCCC TTTTGTGTA | 840 |
| AGCAGAAAGG GAGCTGTGAG CCTTGCCCTG TTTGCAGGTG TCAAGTGCCT CTCCCTGCCT | 900 |
| GTAATTCTCC CCTTCCTCTG AGCAGAGCTT TGGTAGCTGT TGCCAATGCA AAGAAATGTA | 960 |
| AAGCAGCAAA AGAAGACAGC AGGTTCCTGAC CTGAGGAGGG AAACCAAAT TATCCACAA | 1020 |
| AGGCCCATTA ACCCACCCC CCTCGCCTCC CACCCCAGA CTGGATCCAC TACTGGCCCA | 1080 |
| AGAATACTGA TGAGAAACCT AGTCTGGATT GGGTCGGAAG CTGGAATTTG GTGCTCTGCA | 1140 |
| GACCAGTGCT CAAAATTGTG GTTATTTTTG AGGACTCGCC TTCAATCCAG AACATTTGCG | 1200 |
| TTTCACCTTC CTCGCCCAGA TCCAGTTAAC AAGGTAGCTC ATCACTTCTT GCATCTGTTG | 1260 |
| AGTGACATGC TGGATTTTAA TTTTATTGT GGTGTACTT GGATGCAAGG AATATGTTTT | 1320 |
| GTTCTCCCA ATTTAGCGCA CCATCCTGGG AAGTGCATGT CTCAGACCAA CTCCACCTTC | 1380 |
| ACCTTACCA CCTGTGCGAT CCTGCATCCT TCAGATGAGC TCACTCGGGT CACACCAAGC | 1440 |
| CTTAACTCAG CCCCAACTCC AGCTTGTGGC AGCACCAGCC ACTTGAAATC CACGCCGGTG | 1500 |

GCCACACCAT GCACTCCACG GAGACTGAGC CTGGCTGAGT CCTTCACTAA CACCCGTGAG 1560
TCCACGACCA CCATGAGCAC ATCCCTGGGG CTCGTGTGGC TGTGAAGGA GCGGGGCATT 1620
TCTGCTGCCG TGTACGACCC CCAGAGCTGG GACAGGGCCG GCCGGGGCTC CCTCCTGCAC 1680
TCCTACACGC CCAAGATGGC TGTGATCCCC TCTACTCCGC CGAACTCGCC TATGCAGACA 1740
CCCACATCCT CCCACCCCTC CTTTGAGTTC AAGTGCACGA GCCCTCCCTA CGACAATTTC 1800
CTGGCTTCCA AGCCAGCCAG CTCCATCCTG AGGGAAGTGA GAGAAAAGAA CGTCCGCAGC 1860
AGCGAGAGCC AGACCGACGT GTCCGTCTCC AACCTCAACC TCGTGGACAA AGTCAGGAGG 1920
TTTGGGGTGG CCAAAGTGGT GAACTCAGGG CGAGCCCATG TCCCCACCTT GACTGAGGAG 1980
CAGGGACCCC TCCTCTGTGG GCCCCCGGGG CCAGCACCAG CCCTTGTTCC CAGAGGCCTG 2040
GTACCTGAGG GCCTGCCCCT CAGATGCCCC ACTGTCACCA GTGCCATCGG TGGGCTGCAG 2100
CTCAATAGTG GCATCCGGCG GAATCGCAGC TTCCCCACCA TGGTGGGATC TAGCATGCAG 2160
ATGAAAGCTC CTGTGACTCT CACCTCGGGC ATCTTGATGG GTGCTAAGCT CTCCAAACAA 2220
ACTAGCTTAC GGTGAGGACT GGAGGGGGGC CGGTTGCCCT AGAGGAGACC CACGTTCTCT 2280
CTTGCTCCCA CCTCCCTCTC TTCCCCCAC AGTGCCTCC CTCCCTCTGC CCTTCTCTGT 2340
CCACCCCTC CTAAGCTAGA CAAATCAACC TTGTGCCTAA TGGAGGAAGT GTGGAAACTT 2400
TGTAATGT GTACATAGGA CTTGGAGACC TTGTGTCCGC CTGCTCTTT CTTCCGATCC 2460
CACAGGAAGT GCCCTGCAC TGTATCACT CTCACGAGGA CGTCACCTGT GCTAACCTGG 2520
GGGAAGGTGG GGTCTTTCT TCTTTCCTT TGAGAAGCAC TGAAACTCCC AAGTGTGTTC 2580
TTATCCCATG GATAGGAAAC CAGTGAATTC CGTGGCTGGC ACACCACGAG CTGTCATGCG 2640
GCACGGGTCA TAACACATCT GGGTGTATC GGACACCTCA CCTCGCCAC CCTGTAGGAG 2700
CGTAAGGAGC CTCCATCCTC AGCCACGTGC AGCTGACGTG GCTTTCCTGA TCGGAGGGCT 2760
TTTCTTTTAT GGGTGGCCCA GCTTCTTCAA GACCTTCACT GCTCTGCCTC AGTGGACAGT 2820
CGTTTCTTTT TTGAGGTGTG ACCTTTTGTT TTCATGCCTT CCCCTGAAG TCATCCTGTG 2880
TTTTGTAATC AGCTGTCAGG CCAAATGTCT GACCCGAAAG AGAATGTATT TACACTCATG 2940
CTGCGTTGTT CAGCAGCCCC TCTGTGTTCT GTGTGATTTG TTTTATTTTT CCTTTTTTTT 3000
ACATATATAT GCAGGGAAGT AATGGTACTG GTAGTGTATG TTTTCTATGT GGTCAAATA 3060
TGAATTTTGA ACACACCAAG CCGCTAATGA GATAGCAGCT TTTTCTGGG ACCCAGAGTC 3120
ACAACCAAAT TGATTTAAGA CCGGACCCAA GACACCTTTA ACAATAGGAC TGAAAGGAAA 3180
AAGGATAGGG AAAAAGCTTA TTAAAGAAAT GTGTCAACAC CAAATGTAGA GGGGAAGAAC 3240

CACAACCAGG CATAATACCA AACCGGTTCC AGGGGGAAAC AAGGCTTTGG TATTCCGCTG 3300
GCTCCAGCGC TTTTCTGAA ACCCGAGGCT GGCCAGGGTG CTGTCACCGT GTGGTCTTTG 3360
ATTGCAGCCA TTCAATGCCC ACATGCTTTT CCTTCTTGTT TCAGAACAGC ACATGGTCAC 3420
AACAAGATAT TTTCTTTCCC TCCAAAGCCT TTTGTCTCCT TGTGCCTCTT TTTATCCTTA 3480
GGAAAAGATC CAGGTGCTTG TGAAAAGAAT CATGAATGCA ACAAGGGAGG CTGGTCCTGT 3540
TGCTGTGCGC GATTAAGTTT TAAACTTTTA TTTATTATTT ATGTCTGCCG TATTTTAAAT 3600
AAACATTCTC GTTCCTTCCA GTTCAGTCA TAGTGTGTCT GTGGCATTCC AGTCCAACCA 3660
TGTGACTTAT TTATTCTAAT TTGAGGGCTG CACTGTACAC CATGGTGTCC TGTGACACCG 3720
TGTTCCAGAC ATTTATGGAA GGAAAACATC CCATATAAAT GAAACTGTCA TGCTGTGTCC 3780
TCCCCGGCAG CAGAAGATGT GTCCTTCCAT TGAGTGAGGG TAACCTTATG TCCACCAAGG 3840
ATACTTTGAG AAAGCCCCTA AGGAACAAGC CTCAGTCCCA CGGTTTCAGA CTATTTATTC 3900
TCTGAACACA AGAGTATTGG TTAATTATGT TCTCAGCTCT CCCTGCTGTT GTATGTGTGC 3960
ATTCACTGCA AGTAACTTAT ATCTTTTTAT TTGAATGTAT TTTAAAGCAG TAGATAGAAT 4020
AACAAAGGAA TATGAAAACC ATGGACTGAA TGGACCATT TATGTATTCA GAGAGAGAAG 4080
CCACTCATCA TTGCCAGAAA TACCATGTAA AAATTGGCAG TTCAGAGGTT GCAATACTTA 4140
GTATAGTAAA TAAATAAACG GTCAACATTG TGCAACCACT ACCAAAAAGT GTGTTGTAAT 4200
GCATCAAAAA TCAACACAAT TTTATTCACT AATGAGTATC AATAAAATAA GTTCAAATGA 4260
TGGAAACCAC AAAAAAAAAA AAAAA 4285

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Met Gln Arg Asn Val Lys Gln Gln Lys Lys Thr Ala Gly Ser Asp Leu
1 5 10 15
Arg Arg Glu Thr Lys Phe Ile Pro Gln Arg Pro Ile Asn Pro Thr Pro
20 25 30
Leu Ala Ser His Pro Gln Thr Gly Ser Thr Thr Gly Pro Arg Ile Leu

| 35 | | | | | 40 | | | | | 45 | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Asn | Leu | Val | Trp | Ile | Gly | Ser | Glu | Ala | Gly | Ile | Trp | Cys | Ser |
| 50 | | | | | | 55 | | | | | 60 | | | | |
| Ala | Asp | Gln | Cys | Ser | Lys | Leu | Trp | Leu | Phe | Leu | Arg | Thr | Arg | Leu | Gln |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Ser | Arg | Thr | Phe | Ala | Phe | His | Leu | Pro | Arg | Pro | Asp | Pro | Val | Asn | Lys |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Val | Ala | His | His | Phe | Leu | His | Leu | Leu | Ser | Asp | Met | Leu | Asp | Phe | Asn |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Phe | Tyr | Cys | Gly | Cys | Thr | Trp | Met | Gln | Gly | Ile | Cys | Phe | Val | Pro | Pro |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Asn | Leu | Ala | His | His | Pro | Gly | Lys | Cys | Met | Ser | Gln | Thr | Asn | Ser | Thr |
| | | | | | | 135 | | | | | 140 | | | | |
| Phe | Thr | Phe | Thr | Thr | Cys | Arg | Ile | Leu | His | Pro | Ser | Asp | Glu | Leu | Thr |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Arg | Val | Thr | Pro | Ser | Leu | Asn | Ser | Ala | Pro | Thr | Pro | Ala | Cys | Gly | Ser |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Thr | Ser | His | Leu | Lys | Ser | Thr | Pro | Val | Ala | Thr | Pro | Cys | Thr | Pro | Arg |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Arg | Leu | Ser | Leu | Ala | Glu | Ser | Phe | Thr | Asn | Thr | Arg | Glu | Ser | Thr | Thr |
| | | | 195 | | | | 200 | | | | | 205 | | | |
| Thr | Met | Ser | Thr | Ser | Leu | Gly | Leu | Val | Trp | Leu | Leu | Lys | Glu | Arg | Gly |
| | | | | | | 215 | | | | | 220 | | | | |
| Ile | Ser | Ala | Ala | Val | Tyr | Asp | Pro | Gln | Ser | Trp | Asp | Arg | Ala | Gly | Arg |
| 225 | | | | | | 230 | | | | | 235 | | | | 240 |
| Gly | Ser | Leu | Leu | His | Ser | Tyr | Thr | Pro | Lys | Met | Ala | Val | Ile | Pro | Ser |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Thr | Pro | Pro | Asn | Ser | Pro | Met | Gln | Thr | Pro | Thr | Ser | Ser | Pro | Pro | Ser |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Phe | Glu | Phe | Lys | Cys | Thr | Ser | Pro | Pro | Tyr | Asp | Asn | Phe | Leu | Ala | Ser |
| | | | 275 | | | | 280 | | | | | 285 | | | |
| Lys | Pro | Ala | Ser | Ser | Ile | Leu | Arg | Glu | Val | Arg | Glu | Lys | Asn | Val | Arg |
| | | | | | | 295 | | | | | 300 | | | | |
| Ser | Ser | Glu | Ser | Gln | Thr | Asp | Val | Ser | Val | Ser | Asn | Leu | Asn | Leu | Val |
| 305 | | | | | | 310 | | | | | 315 | | | | 320 |
| Asp | Lys | Val | Arg | Arg | Phe | Gly | Val | Ala | Lys | Val | Val | Asn | Ser | Gly | Arg |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Ala | His | Val | Pro | Thr | Leu | Thr | Glu | Glu | Gln | Gly | Pro | Leu | Leu | Cys | Gly |

| | | |
|---|-------------------------------------|-----|
| 340 | 345 | 350 |
| Pro Pro Gly Pro Ala Pro Ala | Leu Val Pro Arg Gly Leu Val Pro Glu | |
| 355 | 360 | 365 |
| Gly Leu Pro Leu Arg Cys Pro Thr Val Thr Ser Ala Ile Gly Gly Leu | | |
| 370 | 375 | 380 |
| Gln Leu Asn Ser Gly Ile Arg Arg Asn Arg Ser Phe Pro Thr Met Val | | |
| 385 | 390 | 395 |
| Gly Ser Ser Met Gln Met Lys Ala Pro Val Thr Leu Thr Ser Gly Ile | | |
| 405 | 410 | 415 |
| Leu Met Gly Ala Lys Leu Ser Lys Gln Thr Ser Leu Arg | | |
| 420 | 425 | |

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3751 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

| | |
|--|-----|
| ACTTTGAATT TTTTATTTGT GAAATTAAAA ATATGGTATT ATATATATAT AAACCTCTAT | 60 |
| TCCTCTATAA ATATAGATGA TTTTGTGATA GTGAACAGAA TAAATGTATA CCAAATTCAA | 120 |
| AGACCAATAT CATTTTAGCG TATGACAGAC ATAGATAAAT TTAGGTCCTA AGTACCGGCA | 180 |
| TTTTGATAAA TTCTTAAAGT TTAAAACAAT ACAATCAGGA GGATTGCTTT TCTCCTCTTC | 240 |
| TTCACAGAGA ACTAAAGTGA ATATTTTAA ATGGCTTTGA AAGATTTACA TTTGACACAT | 300 |
| TTCTGTAAAT CAAAAGAGG AGCACACAGG GATTTAATGC AGTAGACCTG CACACATTTT | 360 |
| CCCTTTAGCA TGCATGCCCA TATTTTGTTT ATTTCAAGGCG CTATCTCCCC GTCAATTATT | 420 |
| CCACCTTCTT TACCTCCTGA AATCTTACCA GGTATTATT GGTGGTGTGA ATTGTTCCCC | 480 |
| CCTCAGAATG TGCTGCTGAA TAATAATCGT AATAAAATGT TGAAAGTGTA CAACTTTTAC | 540 |
| ATTTTAAAGT TTCTGATATA TGTCTAGTTA TTTGATTAAA AATAAGAAAA TAGCACTTCA | 600 |
| TTTTGAGGAA GTCCATGACA CTGAAATATC CTTCAAGTTT TCAATTTCTG TTTACGTTTT | 660 |
| GCTGTCTTGT TAAGGAAAGC AAACATCAAC TCCTTAACAA AGCTTCCAG GTGACCTCAA | 720 |
| CATTTCCATT TTACAGACCG GTAAAATCTA AGCGCAGGCT GTCTCATTCT CAAAGGCAAG | 780 |
| GTTGCCAGGC ATCCGTATGC AATTAGAATT AACATTTTAT AACCCATATC TTCAGTCTCT | 840 |

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|------|
| TCCAACCCAC | ACAAAGCTTC | ATGCTTCTTC | CCAAATCTCA | GTAACCACAT | CTTTCCATGA | 900 |
| CGCTGGCCAA | ACCCATACCA | GGTTTTAGAC | ACTAGAGAAT | GAAATGAGCT | CACCCCTCAA | 960 |
| AAATTAGACT | TCAAAAAGTT | TGGCATTGGT | TATCTCACTC | ACCCTGTAAC | CAACTAAGGT | 1020 |
| GGGAGAAGGG | AGTGTCTGGC | GTTGAAGGTG | ACCGTGGAGG | GAGGCTGAGA | CTGCCAGCGC | 1080 |
| CCACACCCGT | GGGCCCCCAT | GAAGTTGGAG | GAAAGTTCTG | GACAGTTAAA | AATCCAGCTT | 1140 |
| CAGGAAGTCG | AAGGGACGGG | CCTTCGCAAT | CCACCGCCGA | GCAAGGGAGG | AATTGTAATG | 1200 |
| TATGGGGGCC | CTCCTCCAGA | TTTGGAAGGT | TTGTGGAGTT | CTGTACCTTA | AGAGCCCCTA | 1260 |
| CCTCAAGCCA | GGAAAGAAAG | GGAGGGGACA | GAAGGAGGGG | GAGGGGGCAA | AAGGAGGAGG | 1320 |
| CGGGAAGTGA | CCCTGGCAGC | GCAGCCCTAG | TCGCACCCCG | CAGTGCTGAA | CTCGCCCCGG | 1380 |
| AGCTGGCGCC | CAGCCGTCCC | GAGCACCCGT | GGTAGGGAGA | GGCGCGCGAG | GACGACCAGG | 1440 |
| AGCGCTGTGC | GGTTGCACAC | CAGTTTTAGC | TCCTTTGCAA | TACTCCGAAA | AGGGCAAGAA | 1500 |
| GAAAAGCCTC | AAATGGTTAA | ACCGCCCTAA | ATAATTAAAA | ACTTTTGAAA | AAGAAAAACG | 1560 |
| CGTGATCGGT | CGTCATTTAA | ATACAAATAT | ACTTACAAAA | ATCCTACACA | GGCTATTTAC | 1620 |
| AATCATAAAA | GCGAACAGTC | CTGGTACCAG | AGTGTGAGGG | CAAGAGGTCT | GTCCATCCTC | 1680 |
| CCTCTGGCAG | TCGGGCCCTC | GTGTCTTTTT | GCCTCAGGGA | CGGAAGCTTT | TGCAGGAGCT | 1740 |
| GAGTTGTTCT | AGGCCTCTTT | GGCCGAATTC | GGCCAAAGAG | GCCTAATTCC | TTCCTCGGTT | 1800 |
| ATTTCAITCA | GAGAATATTT | ATGAAATGCC | TACTGTGTGC | AAGTCATCCA | TCCTTGAAAA | 1860 |
| GGCCACTTCT | CAGTGAGGGA | GAGATGTAGT | GGATTCTGTG | AGACATACCT | GCTGGAGTTG | 1920 |
| AAGCAGTAAA | TAGCATGTCT | TTCCCCCTCC | CGATCTTAAG | GTGTGTTTTTC | TAGAAAAGTT | 1980 |
| CCCTAATGGA | ATTCATGAGT | TTGGGGGTCT | CAGTCACCCG | CTTGCCTGTA | GGATTCCATT | 2040 |
| TGATGATTCT | GGATTTTTGC | TGTTTGTTAT | TGCCCTTAGA | GGGGCTCTGA | GTATCTACTT | 2100 |
| GTGGGTGGCC | ATTTCTTGAC | ATCTGCATGT | ACCTCGTGGA | ATTCAGCCAG | CTTCATGTTG | 2160 |
| CAAATCAGAA | AGCTGACCCC | AAGACTGCAA | ATCAATGAAG | GTATTGGCAT | TGTTAAGGTC | 2220 |
| GTAGCGTAGA | CAACAGCAGT | CATAAATAAT | TAGGCAGGAA | CTTAACCCAA | ATCTAGTTCT | 2280 |
| TTGACCACCT | CTACCACCAG | AACCCAGCAG | ACACTCACAT | CTCCTGATAA | GAGTTGCTGG | 2340 |
| ACTCGATGTT | TTTGTTTTGC | ATTTTCTCCT | CTCCTTCCCC | ACTTACTCAG | AGAATTTAAA | 2400 |
| GTCTGTAGAG | TCAGCACAGC | CCCATCAGTC | CAGGAACTTC | CCACCACCAG | CCCTTGACTG | 2460 |
| TCCCATTAAC | TGACATGGTC | AGATTTCCAG | CTCCCCCTAC | TCCCTGCTGT | GAAACAATCC | 2520 |

| | |
|--|------|
| CTCTCCYTGT GAGAGGAAAY TGC GCGSGAA GGYTAAGGGA GTGTGGCGGG CGGYTCCGGG | 2580 |
| AGCCAACATG CCTCGGTATG CGCAGCTGKT CATGGSCCCC GCGGGCAGCG GGAAGAGCAC | 2640 |
| Y TACTGTGCC ACCATGGTCC AGCACTGTGA AGCCYTCAAC CGGTCTGTCC AAGTTGTAAA | 2700 |
| CCTGGATCCA GCAGCAGAAC ACTTCAAYTA CTCCGTGATG GCTGACATCC GGGAACTGAT | 2760 |
| CGAGGTGGAT GATGTAATGG AGGATGATTY TYTGCGATTC GGTCCCAACG GAGGATTGGT | 2820 |
| ATTTTGCATG GAGTACTTTG CCAATAATTT T GACTGGCTG GAGAACTGTC TTGGCCATGT | 2880 |
| AGAGGACGAC TATATCCTTT TTGATTGTCC AGGTCAGATT GAGTTGTACA CTCACCTGCC | 2940 |
| TGTGATGAAA CAGCTGGTCC AGCAGCTCGA GCAGTGGGAG TTCCGAGTCT GTGGAKTTY | 3000 |
| TYTTGTTGAT TCTCAGTTCA TGGTGGAGTC ATTCAAGTTT ATTTCTGGCA TCTTGGCAGC | 3060 |
| CCTGAGTGCC ATGATCTCTC TAGAAATTCC GCAAGTCAAC ATCATGACAA AAATGGATCT | 3120 |
| GCTGAGTAAA AAAGCAAAAA AGGAAATTGA GAAATTTTTA GATCCAGACA TGTATTCTTT | 3180 |
| ATTAGAAGAT TCTACAAGTG ACTTAAGAAG CAAAAAATTC AAGAACTGA CTAAAGCTAT | 3240 |
| ATGTGGACTG ATTGATGACT ACAGCATGGT TCGATTTTTA CCTTACGATC AGTCAGATGA | 3300 |
| AGAAAGCATG AACATTGTAT TGCAGCATAT TGATTTTGCC ATTCAATATG GAGAAGACCT | 3360 |
| AGAATTTAAA GAACCAAAGG AACGTGAAGA TGAGTCTTCC TCTATGTTTG ACGAATATTT | 3420 |
| TCAAGAATGC CAGGATGAAT GAAGAGTTTA CTAAAAGTAA CCATCTAAAG AGCTTGTTGC | 3480 |
| CAAACCAGCA GAACATTCTT CTYTTCAAAG GATGCAATAG TAGAAAGCTA CTTATTTTAA | 3540 |
| TGAAAAAAG TAAAACTTCG TTCTTTATCA GCCTCATGCC TGAATCAAAT TTTTAATTAT | 3600 |
| TCTGAAACTG CTGCTGTTTA AAGTGAATC TTTTAGTATT ATAACAGCAT CACTTTAGAT | 3660 |
| TTTGTAAGTC AAAATTGAAA TGAATGCACA TAGATTTATA TATAAATTAG CACCTGAGCT | 3720 |
| AAAAAAAAA AAAAAAAAAA AAAAAAAAAA A | 3751 |

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Met Pro Arg Tyr Ala Gln Leu Xaa Met Xaa Pro Ala Gly Ser Gly Lys

| | | | |
|---|-----|-----|-----|
| 1 | 5 | 10 | 15 |
| Ser Thr Tyr Cys Ala Thr Met Val Gln His Cys Glu Ala Xaa Asn Arg | 20 | 25 | 30 |
| Ser Val Gln Val Val Asn Leu Asp Pro Ala Ala Glu His Phe Asn Tyr | 35 | 40 | 45 |
| Ser Val Met Ala Asp Ile Arg Glu Leu Ile Glu Val Asp Asp Val Met | 50 | 55 | 60 |
| Glu Asp Asp Xaa Leu Arg Phe Gly Pro Asn Gly Gly Leu Val Phe Cys | 65 | 70 | 75 |
| Met Glu Tyr Phe Ala Asn Asn Phe Asp Trp Leu Glu Asn Cys Leu Gly | 85 | 90 | 95 |
| His Val Glu Asp Asp Tyr Ile Leu Phe Asp Cys Pro Gly Gln Ile Glu | 100 | 105 | 110 |
| Leu Tyr Thr His Leu Pro Val Met Lys Gln Leu Val Gln Gln Leu Glu | 115 | 120 | 125 |
| Gln Trp Glu Phe Arg Val Cys Gly Xaa Xaa Xaa Val Asp Ser Gln Phe | 130 | 135 | 140 |
| Met Val Glu Ser Phe Lys Phe Ile Ser Gly Ile Leu Ala Ala Leu Ser | 145 | 150 | 155 |
| Ala Met Ile Ser Leu Glu Ile Pro Gln Val Asn Ile Met Thr Lys Met | 165 | 170 | 175 |
| Asp Leu Leu Ser Lys Lys Ala Lys Lys Glu Ile Glu Lys Phe Leu Asp | 180 | 185 | 190 |
| Pro Asp Met Tyr Ser Leu Leu Glu Asp Ser Thr Ser Asp Leu Arg Ser | 195 | 200 | 205 |
| Lys Lys Phe Lys Lys Leu Thr Lys Ala Ile Cys Gly Leu Ile Asp Asp | 210 | 215 | 220 |
| Tyr Ser Met Val Arg Phe Leu Pro Tyr Asp Gln Ser Asp Glu Glu Ser | 225 | 230 | 235 |
| Met Asn Ile Val Leu Gln His Ile Asp Phe Ala Ile Gln Tyr Gly Glu | 245 | 250 | 255 |
| Asp Leu Glu Phe Lys Glu Pro Lys Glu Arg Glu Asp Glu Ser Ser Ser | 260 | 265 | 270 |
| Met Phe Asp Glu Tyr Phe Gln Glu Cys Gln Asp Glu | 275 | 280 | |

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

TNCAGGCCTT GCGTTCCTAG CTGCTCTGC

29

- (2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GNGCTGTGAG TTTATCCACA AAGGAACAG

29

- (2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GNATAGGAGG TCCCAAGTTA TCAAGGTTT

29

- (2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

GNTTTCCTGG TTCTTGGTCA GGTTCCTC

29

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

CNAGATGCAA TGGTTGTGAG ATTGACCAA

29

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

GNCACTTCC ACTGCTGTGA GCTTGTCAT

29

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

ANCAGACAGT TTGCCATGGA GTACATCAC

29

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

TNATGAACCA CAGGAAACAG GAAGCCGTC

29

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

TNAAGGTGAA GGTGGAGTTG GTCTGAGAC

29

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GNCAGAAATA AACTTGAATG ACTCCACCA

29

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS :

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Met Asn Ser Gln Leu Asn Ser Phe Thr Gly Gln Met Glu Asn Ile Thr
1 5 10 15

Thr Ile Ser Gln Ala Asn Glu Gln Asn Leu Lys Asp Leu Gln Asp Leu
20 25 30

His Lys Asp Ala Glu Asn Arg Thr Ala Ile Lys Phe Asn Gln Leu Glu
35 40 45

Glu Arg Phe Gln Leu Phe Glu Thr Asp Ile Val Asn Ile Ile Ser Asn
50 55 60

Ile Ser Tyr Thr Ala His His Leu Arg Thr Leu Thr Ser Asn Leu Asn
65 70 75 80

Glu Val Arg Thr Thr Cys Thr Asp Thr Leu Thr Lys His Thr Asp Asp
85 90 95

Leu Thr Ser Leu Asn Asn Thr Leu Ala Asn Ile Arg Leu Asp Ser Val
100 105 110

Ser Leu Arg Met Gln Gln Asp Leu Met Arg Ser Arg Leu Asp Thr Glu
115 120 125

Val Ala Asn Leu Ser Val Ile Met Glu Glu Met Lys Leu Val Asp Ser
130 135 140

Lys His Gly Gln Leu Ile Lys Asn Phe Thr Ile Leu Gln Gly Pro Pro
145 150 155 160

Gly Pro Arg Gly Pro Arg Gly Asp Arg Gly Ser Gln Gly Pro Pro Gly
165 170 175

Pro Thr Gly Asn Lys Gly Gln Lys Gly Glu Lys Gly Glu Pro Gly Pro
180 185 190

Pro Gly Pro Ala Gly Glu Arg Gly Pro Ile Gly Pro Ala Gly Pro Pro
195 200 205

Gly Glu Arg Gly Gly Lys Gly Ser Lys Gly Ser Gln Gly Pro Lys Gly
210 215 220

Ser Arg Gly Ser Pro Gly Lys Pro Gly Pro Gln Gly Pro Ser Gly Asp
225 230 235 240

Pro Gly Pro Pro Gly Pro Pro Gly Lys Glu Gly Leu Pro Gly Pro Gln
245 250 255

Gly Pro Pro Gly Phe Gln Gly Leu Gln Gly Thr Val Gly Glu Pro Gly
260 265 270

Val Pro Gly Pro Arg Gly Leu Pro Gly Leu Pro Gly Val Pro Gly Met
275 280 285

Pro Gly Pro Lys Gly Pro Pro Gly Pro Pro Gly Pro Ser Gly Ala Val
290 295 300

Val Pro Leu Ala Leu Gln Asn Glu Pro Thr Pro Ala Pro Glu Asp Asn
305 310 315 320

Ser Cys Pro Pro His Trp Lys Asn Phe Thr Asp Lys Cys Tyr Tyr Phe
325 330 335

Ser Val Glu Lys Glu Ile Phe Glu Asp Ala Lys Leu Phe Cys Glu Asp
340 345 350

Lys Ser Ser His Leu Val Phe Ile Asn Thr Arg Glu Glu Gln Gln Trp
355 360 365

Ile Lys Lys Gln Met Val Gly Arg Glu Ser His Trp Ile Gly Leu Thr
370 375 380

Asp Ser Glu Arg Glu Asn Glu Trp Lys Trp Leu Asp Gly Thr Ser Pro
385 390 395 400

Asp Tyr Lys Asn Trp Lys Ala Gly Gln Pro Asp Asn Trp Gly His Gly
405 410 415

His Gly Pro Gly Glu Asp Cys Ala Gly Leu Ile Tyr Ala Gly Gln Trp
420 425 430

Asn Asp Phe Gln Cys Glu Asp Val Asn Asn Phe Ile Cys Glu Lys Asp
435 440 445

Arg Glu Thr Val Leu Ser Ser Ala Leu
450 455

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Cys Gly His His Glu Leu Asn Asn Leu Asn Leu Thr Gln Val Gln Gln
1 5 10 15

Arg Asn Leu Ile Thr Asn Leu Gln Arg Ser Val Asp Asp Thr Ser Gln
20 25 30

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Ala | Ile | Gln | Arg | Ile | Lys | Asn | Asp | Phe | Gln | Asn | Leu | Gln | Gln | Val | Phe | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | |
| Leu | Gln | Ala | Lys | Lys | Asp | Thr | Asp | Trp | Leu | Lys | Glu | Lys | Val | Gln | Ser | | |
| | | 50 | | | | 55 | | | | | 60 | | | | | | |
| Leu | Gln | Thr | Leu | Ala | Ala | Asn | Asn | Ser | Ala | Leu | Ala | Lys | Ala | Asn | Asn | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | |
| Asp | Thr | Leu | Glu | Asp | Met | Asn | Ser | Gln | Leu | Asn | Ser | Phe | Thr | Gly | Gln | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | |
| Met | Glu | Asn | Ile | Thr | Thr | Ile | Ser | Gln | Ala | Asn | Glu | Gln | Asn | Leu | Lys | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | |
| Asp | Leu | Gln | Asp | Leu | His | Lys | Asp | Ala | Glu | Asn | Arg | Thr | Ala | Ile | Lys | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | |
| Phe | Asn | Gln | Leu | Glu | Glu | Arg | Phe | Gln | Leu | Phe | Glu | Thr | Asp | Ile | Val | | |
| | | 130 | | | | 135 | | | | | 140 | | | | | | |
| Asn | Ile | Ile | Ser | Asn | Ile | Ser | Tyr | Thr | Ala | His | His | Leu | Arg | Thr | Leu | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | |
| Thr | Ser | Asn | Leu | Asn | Glu | Val | Arg | Thr | Thr | Cys | Thr | Asp | Thr | Leu | Thr | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | |
| Lys | His | Thr | Asp | Asp | Leu | Thr | Ser | Leu | Asn | Asn | Thr | Leu | Ala | Asn | Ile | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | |
| Arg | Leu | Asp | Ser | Val | Ser | Leu | Arg | Met | Gln | Gln | Asp | Leu | Met | Arg | Ser | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | | |
| Arg | Leu | Asp | Thr | Glu | Val | Ala | Asn | Leu | Ser | Val | Ile | Met | Glu | Glu | Met | | |
| | | 210 | | | | 215 | | | | | 220 | | | | | | |
| Lys | Leu | Val | Asp | Ser | Lys | His | Gly | Gln | Leu | Ile | Lys | Asn | Phe | Thr | Ile | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | |
| Leu | Gln | Gly | Pro | Pro | Gly | Pro | Arg | Gly | Pro | Arg | Gly | Asp | Arg | Gly | Ser | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | |
| Gln | Gly | Pro | Pro | Gly | Pro | Thr | Gly | Asn | Lys | Gly | Gln | Lys | Gly | Glu | Lys | | |
| | | | 260 | | | | | 265 | | | | | 270 | | | | |
| Gly | Glu | Pro | Gly | Pro | Pro | Gly | Pro | Ala | Gly | Glu | Arg | Gly | Pro | Ile | Gly | | |
| | | 275 | | | | | 280 | | | | | 285 | | | | | |
| Pro | Ala | Gly | Pro | Pro | Gly | Glu | Arg | Gly | Gly | Lys | Gly | Ser | Lys | Gly | Ser | | |
| | | 290 | | | | 295 | | | | | 300 | | | | | | |
| Gln | Gly | Pro | Lys | Gly | Ser | Arg | Gly | Ser | Pro | Gly | Lys | Pro | Gly | Pro | Gln | | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | | |
| Gly | Pro | Ser | Gly | Asp | Pro | Gly | Pro | Pro | Gly | Pro | Pro | Gly | Lys | Glu | Gly | | |
| | | | | 325 | | | | | 330 | | | | | 335 | | | |

Leu Pro Gly *Pro Gln Gly Pro Pro Gly Phe Gln Gly Leu Gln Gly Thr
 340 345 350
 Val Gly Glu Pro Gly Val Pro Gly Pro Arg Gly Leu Pro Gly Leu Pro
 355 360 365
 Gly Val Pro Gly Met Pro Gly Pro Lys Gly Pro Pro Gly Pro Pro Gly
 370 375 380
 Pro Ser Gly Ala Val Val Pro Leu Ala Leu Gln Asn Glu Pro Thr Pro
 385 390 395 400
 Ala Pro Glu Asp Asn Ser Cys Pro Pro His Trp Lys Asn Phe Thr Asp
 405 410 415
 Lys Cys Tyr Tyr Phe Ser Val Glu Lys Glu Ile Phe Glu Asp Ala Lys
 420 425 430
 Leu Phe Cys Glu Asp Lys Ser Ser His Leu Val Phe Ile Asn Thr Arg
 435 440 445
 Glu Glu Gln Gln Trp Ile Lys Lys Gln Met Val Gly Arg Glu Ser His
 450 455 460
 Trp Ile Gly Leu Thr Asp Ser Glu Arg Glu Asn Glu Trp Lys Trp Leu
 465 470 475 480
 Asp Gly Thr Ser Pro Asp Tyr Lys Asn Trp Lys Ala Gly Gln Pro Asp
 485 490 495
 Asn Trp Gly His Gly His Gly Pro Gly Glu Asp Cys Ala Gly Leu Ile
 500 505 510
 Tyr Ala Gly Gln Trp Asn Asp Phe Gln Cys Glu Asp Val Asn Asn Phe
 515 520 525
 Ile Cys Glu Lys Asp Arg Glu Thr Val Leu Ser Ser Ala Leu
 530 535 540